

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2002, 23:43:29 ; Search time 237.55 Seconds

(without alignments)
8991.124 Million cell updates/sec

Title: US-09-723-676-1

Perfect score: 1244
1 gttgtctcactcgtcagtc.....gcattctcctaactctaa 1244

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1244	100.0	1244	22	AAD08531	Human Interleukin-
2	537.4	43.2	585	22	AAC90487	Human IL-1 eta CDN
3	459	36.9	520	22	AAE83869	Human Interleukin-
4	324.4	26.1	1190	19	AAV69326	Human IL-1 delta c
5	273	21.9	1304	23	AA594214	DNA encoding novel
6	251.8	20.2	320	19	AAV69327	Human IL-1 delta c
7	134.2	10.8	477	21	AA551247	Human Interleukin-
8	134.2	10.8	477	21	AA551248	Polymorphic human
9	132	10.6	819	22	AAD06911	Human Interleukin-

10	126.4	10.2	1073	22	AAD12296	Human interleukin-
11	126.4	10.2	1183	19	AAV42659	CDNA encoding inte
12	126.4	10.2	1183	20	AAV90135	Human interleukin-
13	126.4	10.2	1183	22	AA526842	Human CDNA encodin
14	126.4	10.2	1291	20	AA586458	CDNA encoding a hu
15	126.4	10.2	1377	20	AA586459	CDNA encoding a hu
16	119	9.6	673	22	AA526915	Human CDNA encodin
17	119	9.6	673	22	AAD16762	Human novel protei
18	106.8	8.6	811	23	AA594212	DNA encoding novel
19	104.8	8.4	1321	21	AA596351	CDNA encoding a no
20	104.8	8.4	1321	21	AA515950	Human IL-1 recepto
21	100.8	8.1	809	19	AAV1960	Human IL-1 recepto
22	100.8	8.1	838	20	AA586460	CDNA encoding a mu
23	95.6	7.7	391	22	AAE83870	Human Interleukin-
24	76.2	6.1	654	21	AAD00214	Human zll144-E200K
25	74.6	6.0	654	21	AAD00213	Human zll144 degen
26	74.2	6.0	771	23	AA594215	DNA encoding novel
27	73.2	5.9	531	22	AAE85156	Nucleotide sequenc
28	73.2	5.9	603	22	AAE85157	Nucleotide sequenc
29	73.2	5.9	1577	19	AAV21578	Equine Interleukin
30	73.2	5.9	1614	22	AAE85155	Nucleotide sequenc
31	72.4	5.8	531	17	AAT13177	Human Interleukin-
32	72.4	5.8	557	16	AA089792	IL-1 gene. Homo
33	70.8	5.7	456	14	AA040754	IL-1 inhibitor (IL
34	70.8	5.7	462	18	AAT38808	Recombinant human
35	70.8	5.7	462	19	AAV36455	Human Interleukin-
36	70.8	5.7	462	22	AA170513	Human Interleukin-
37	70.8	5.7	514	16	AA083763	Plasmid 15424. Sy
38	70.8	5.7	514	18	AAT72210	DNA encoding leade
39	70.8	5.7	514	20	AA582158	Leaderless IL-1 re
40	70.8	5.7	531	17	AAT35255	Human Interleukin-
41	70.8	5.7	531	17	AAT30157	Human Interleukin-1 rece
42	70.8	5.7	531	17	AAT30159	Interleukin-1 rece
43	70.8	5.7	532	12	AA014693	IRAP gene. Homo s
44	70.8	5.7	540	10	AA52441	Sequence of bps 61
45	70.8	5.7	543	19	AAV22666	CDNA encoding an i

ALIGNMENTS

RESULT 1	
ID	AAD08531 standard; CDNA; 1244 BP.
XX	XX
AC	AAD08531;
XX	XX
DT	04-SEP-2001 (first entry)
XX	XX
DE	Human Interleukin-1 Receptor Antagonist-Like (IL-1ra-L) CDNA.
XX	XX
KW	Human; Interleukin-1 Receptor Antagonist-Like; IL-1ra-L; atherosclerosis;
KW	multiple sclerosis; septic shock; anorexia; psoriasis; osteoporosis;
KW	emphysema; Alzheimer's disease; gene therapy; tranquiliser; vulnerability;
KW	cytostatic; rheumatoid arthritis; autoimmune disease; diabetes; leprosy;
KW	pulmonary tuberculosis; septicemia; coxidia; hypoglycemia; lung injury;
KW	Parkinson's disease; eczema; glomerulonephritis; haemorrhage; Ischaemia;
KW	leukaemia; infertility; inflammatory eye disease; acute pancreatitis;
KW	fibromyalgia; ss.
OS	Homo sapiens.
XX	XX
FH	Key
FT	Location/Qualifiers
FT	CDS 301..774
FT	/*tag= a
FT	/product= "Human IL-1ra-L protein"
PD	WO200142305-A1.
XX	XX
PD	14-JUN-2001.
XX	XX
PF	28-NOV-2000; 2000MO-US32400.
XX	XX


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PD 30-NOV-2000.
XX
XX 25-MAY-2000; 2000WO-US14435.
XX
XX 25-MAY-1999; 99US-0135758.
PR 29-OCT-1999; 99US-0162331.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Sims JE, Renshaw BR;
PI
XX MPI: 2001-032039/04.
DR P-PSDB; AAB50444.
XX
PT Novel interleukin-1 eta polypeptides useful as therapeutic agents for
PT treatment of diseases mediated by polypeptide counter-structure
PT molecules and for identifying inhibitors -
XX
XX Claim 1; Page 4; 45pp; English.
XX
XX The present sequence encodes an interleukin-1 (IL-1) eta polypeptide.
CC The IL-1 eta polypeptide is useful as a therapeutic agent for the
CC treatment of disease mediated by IL-1 eta polypeptide counter-structure
CC molecules and also for identifying proteins associated with IL-1 eta
CC ligands, to screen for potential inhibitors of activity associated with
CC polypeptide counter-structure molecules and in designing inhibitors.
CC It is used to study cellular processes such as immune regulation, cell
CC proliferation, cell death, cell migration, cell-to-cell interaction and
CC inflammatory responses. IL-1 eta promotes inflammatory responses and is
CC involved in the causation and maintenance of inflammatory and/or
CC autoimmune diseases such as rheumatoid arthritis, inflammatory bowel
CC disease, and psoriasis. IL-1 eta polynucleotides can be used to identify
CC IL-1 eta receptors, to study cell signal transduction and the
CC immune system and to identify genes associated with human conditions
CC such as glaucoma, ectodermal dysplasia, insulin-dependent diabetes
CC mellitus, wrinkly skin syndrome, T-cell leukemia/lymphoma, and tibial
CC muscular dystrophy.
XX
XX Sequence 585 BP; 161 A; 154 C; 110 G; 160 T; 0 other;
SO
Query Match 43.2%; Score 537.4; DB 22; Length 585;
Best Local Similarity 98.0%; Pred. NO. 8-6e-153;
Matches 544; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 220 taacttcgtcgtcctagaaccaccgctcctccaccatcgtatcctgttctctc 279
DB 31 tcaactctcctcactcttctcctagctcctccaccacatcgtatcctgttctctc 90
QY 280 acaaaagctcgaagacatcatgaaccacaaaggaggaagcaaccaccaatcctatgct 339
DB 91 acaaaagctcgaagacatcatgaaccacaaaggaggaagcaaccaccaatcctatgct 150
QY 340 attcgtgattcctgcacagatggtgtggtcctgagtgtgaatctcttaataagcagctcct 399
DB 151 attcgtgattcctgcacagatggtgtggtcctgagtgtgaatctcttaataagcagctcct 210
QY 400 cttaaccggaagattaaagctcgtcactctcttaataagcgtgtagagcacagaattc 459
DB 211 cttaaccggaagattaaagctcgtcactctcttaataagcgtgtagagcacagaattc 270
QY 460 agtgcagaagaaagggtlaatatgttacctggtgaatacaaggaagaaagtctctgtctc 519
DB 271 agtgcagaagaaagggtlaatatgttacctggtgaatacaaggaagaaagtctctgtctc 330
QY 520 ttctgtgcagaattcagggcaagcctactttgcagcttaaggaataatatactatgac 579
DB 331 ttctgtgcagaattcagggcaagcctactttgcagcttaaggaataatatactatgac 390
QY 580 ctgtatgtggaagaaagacagaagcccttctcttccacaataagaagagctcc 639
DB 391 ctgtatgtggaagaaagacagaagcccttctcttccacaataagaagagctcc 450

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QY 640 acttcgtcttcagtcagtcctccttaccctgctggttcatagaccaccaccacatca 699
DB 451 acttcgtcttcagtcagtcctccttaccctgctggttcatagaccaccaccacatca 510
QY 700 ggaacgcccatcttctcaccacaaagagagagcaataactaactaacttactta 759
DB 511 ggaacgcccatcttctcaccacaaagagagagcaataactaactaacttactta 570
QY 760 gattctgtggaataa 774
DB 571 gattctgtggaataa 585
RESULT 3
AAF83869
ID AAF83869 standard; cDNA; 520 BP.
XX
XX AAF83869;
AC
XX 06-AUG-2001 (first entry)
DT
XX
DE Human interleukin-1 receptor antagonist (NOVINTRA B) encoding cDNA.
XX
XX NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW gonadotropin-like protein; NOVGN; interleukin-1; NOVINTRA; human;
KW cytosolic; neuroprotective; reproductive; antiinflammatory; cancer;
KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;
KW antihistaminic; antiallergic; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 3..513
FT CDS /*tag= a
FT /product= "NOVINTRA B"
XX
XX WO200140291-A2.
XX
XX 07-JUN-2001.
XX
XX 06-DEC-2000; 2000WO-US33029.
XX
XX 06-DEC-1999; 99US-0169056.
XX 09-DEC-1999; 99US-0169866.
XX 09-DEC-1999; 99US-0169886.
XX 10-DEC-1999; 99US-0170252.
XX 12-JAN-2000; 2000US-0175740.
XX 05-DEC-2000; 2000US-0170252.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Burgess CE, Prayaga SK, Shinkets RA, Rastelli L, Zehusen BD;
PI Mezes PS;
XX
XX MPI: 2001-374790/39.
XX P-PSDB; AAB85000.
XX
XX Novel isolated human transmembrane, neuromedin peptide
PT gonadotropin-like protein and interleukin-1 receptor antagonist
PT proteins, useful for treating cancer, immune response disorder,
PT metabolic function disorders -
XX
XX Claim 8; Fig 12A; 138pp; English.
XX
XX The invention provides novel polypeptides (NOVX) selected from human
XX transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
XX gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
XX antagonist proteins (NOVINTRA A and B). The invention also provides
XX methods in which a NOVX polypeptide, polynucleotide and antibody are
XX used in the detection, prevention and treatment of a broad range of
XX pathological states. NOVTRAN can be used to treat is a cell signaling
XX disorder such as cancer, immune response disorder, hematopoietic
XX disorder, neurodegenerative disorder. NOVNEUR can be used to treat

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central nervous system, breast, colon, ovary, kidney, prostate and thyroid. NOVSON can be used to treat reproductive development disorder metabolic function disorder and melanoma. NOVINRA A and B can be used to treat bone metabolism or structure disorder, inflammatory response disorder, immune regulation disorder, septic shock, stroke, diabetes, arthritis and cancer. The present sequence represents a cDNA encoding the NOVINRA B polypeptide.

Sequence 520 BP; 147 A; 127 C; 112 G; 134 T; 0 other;

Query Match	36.9%	Score	459	DB	22	Length	520
Best Local Similarity	100.0%	Pred. No.	5.3e-129				
Matches	459	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

QY	323	cacccaactctctatgctatttggtatcttcgcacagatggtgtgtggtcctgtatgtgaaatt	387
Db	62	caccacaattcccaatgctatctcggtatcttcgcacagatggtgtgtgtcctgtatgtgaaatt	121
QY	383	ctttaatagcagctctctctctttagccgcagcatlaagcctgtcaactctcaattaaataagcct	447
Db	122	ctttaatagcagctctctctctttagccgcagcatlaagcctgtcaactctcaattaaataagcct	186
QY	443	gttagagacacaggaatttcaggtgacaaaggaaggtataatggtttacctgggaatcaag	507
Db	182	gttagagacacaggaatttcaggtgacaaaggaaggtataatggtttacctgggaatcaag	241
QY	503	gaaagatcctctgtctctctctctgttcagaagaattccaggcgaacccactttgcagcttaag	567
Db	242	gaaagatcctctgtctctctctctgttcagaagaattccaggcgaacccactttgcagcttaag	301
QY	563	aaaaaataatcatgagacctgtatgtgtgagaagaacagacagaagccctctctcttttcc	622
Db	302	aaaaaataatcatgagacctgtatgtgtgagaagaacagacagaagccctctctcttttcc	361
QY	623	acaaataaggaaggtcccaactctgtcttttaagtaagctcttaaccctggctgtgttaag	682
Db	362	acaaataaggaaggtcccaactctgtcttttaagtaagctcttaaccctggctgtgttttaag	421
QY	683	ccacctccacacatcatgagaaagcccatctttccacacaagagagaagcatataactata	742
Db	422	ccacctccacacatcatgagaaagcccatctttccacacaagagagaagcatataactata	481
QY	743	acactaactctacttagatctctgtgataataatccagc	781
Db	482	acactaactctacttagatctctgtgataataatccagc	520

RESULT 4

ID AAV69326 standard; cDNA; 1190 BP.

AC AAV69326;

DT 08-FEB-1999 (first entry)

Human IL-1 delta cDNA.

KM intolerau-n-1: It-1 delta: human: diagnosis; immunise: vaccine; stroke:
KM inoculate: inflammation; arthritis; septicemia; autoimmune disease;
KM inflammatory bowel disease; psoriasis; transplant rejection; infection;
KM graft versus host disease; ischemia; acute respiratory disease syndrome
KM restenosis; brain injury; AIDS; bone disease; osteoporosis; cancer;
KM lymphoproliferative disorder; arteriosclerosis; Alzheimer's disease;
KM mapping; linkage; ss.

05 Homo sapiens

FH	key	Location/Qualifiers
FT		112..606
FT	CDS	/*tag= a
FT		/product= "IL-1 delta"
FT		

XX EP879889-A2.
 PN
 XX
 XX
 PD 25-NOV-1998.
 XX
 XX
 PE 17-FEB-1998; 98EP-0301169.
 XX
 XX 29-SEP-1997; 97US-0939300.
 PR 19-MAY-1997; 97US-0046957.
 XX
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Connor JR, James IE, Young PR;
 PI
 XX
 DR WPI; 1998-596681/51.
 DR P-PSDB; AAM82542.

Claim 2, Page 17, 21pp: English.
New IL-1 delta polypeptide and polynucleotide- useful as diagnostic reagents and for diagnosing, prevention or treatment of cancer, AIDS or Alzheimer's disease

Claim 2; Page 17; 21pp; English.

This sequence encodes a novel human interleukin-1 polypeptide, IL-1 delta, (interleukin-1 delta). IL-1 delta polypeptides and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the IL-1 delta gene. IL-1 delta antibodies are useful for inducing an immune response to immunise and prevent diseases, and for isolating IL-1 delta clones or purifying the polypeptides by affinity chromatography. IL-1 delta polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, prevented or treated include: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases e.g. inflammatory bowel disease, psoriasis, transplant rejection, graft versus host disease, infection, stroke, ischemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases e.g. osteoporosis, cancer e.g. lymphoproliferative disorders, atherosclerosis and Alzheimer's disease. The IL-1 delta polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis.

Sequence 1190 BP; 371 A; 227 C; 251 G; 341 T; 0 other;

Query Match	26.1%;	Score 324.4;	DB 19;	Length 1190;
Best Local Similarity	96.8%;	Pred. No. 6.4e-88;		
Matches 331; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;

[illegible]

RESULT 5
ID AAS94214
AAS94214 standard; CDNA: 1304 BP.
XX
AC AAS94214;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #30018.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABG30027.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID NO 30018; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1304 BP; 389 A; 293 C; 346 G; 276 T; 0 other;

Query Match 21.9%; Score 273; DB 23; Length 1304;
Best Local Similarity 94.4%; Pred. No. 2.7e-72;
Matches 301; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

OY 243 gctccctcaccaccatcatctatctgttctcttcacaaaaggctcgaagacatcat 302
DB 454 gctccctcaccaccatctgtctatctgttctcttcacaaaaggctcgaagacatcat 513
OY 303 gaaccacaagggagggacacccaatctatgtctatctcgtatcttcgacagatggt 362
|||||

DB 514 gaaccacaacggaggagcagcaccaccaatctatgtctatctgtatcttcgacagatggt 573
OY 363 gtgggtccctagtggaattctttaaagcagctcctcttaagcagacattaaagcctgt 422
DB 574 gtgggtccctagtggaattctttaaagcagctcctcttaagcagacattaaagcct-- 631
OY 423 cactcttaattaaagctgttagacacagaattcagtgacaaaggaaaggaataat 482
DB 632 -----gctgtagagacacagaattcagtgacaaaggaaaggaataat 675
OY 483 ggttacctgggaatcaaggaaaagatctctgtctctctgtgcagaataatcagggcaa 542
DB 676 ggttacctgggaatcaaggaaaagatctctgtctctctgtgcagaataatcagggcaa 735
OY 543 gctcacttgagcagcttaag 561
DB 736 gctcacttgagcagcttaag 754
|||||

RESULT 6
ID AAV69327
AAV69327 standard; CDNA: 320 BP.
XX
AC AAV69327;
XX
DT 08-FEB-1999 (first entry)
XX
DE Human IL-1 delta cDNA fragment.
XX
KW Interleukin-1; IL-1 delta; human; diagnosis; immunise; vaccine; stroke;
KW inoculate; inflammation; arthritis; septicemia; autoimmune disease;
KW inflammatory bowel disease; psoriasis; transplant rejection; infection;
KW graft versus host disease; ischemia; acute respiratory disease syndrome;
KW restenosis; brain injury; AIDS; bone disease; osteoporosis; cancer;
KW lymphoproliferative disorder; atherosclerosis; Alzheimer's disease;
KW mapping; linkage; ss.
XX
KM Homo sapiens.
XX
OS
XX
FH Key Location/Qualifiers
FT 108..320
FT CDS /tag= a
FT /product= "IL-1 delta"
XX
PN EP879889-A2.
XX
PD 25-NOV-1998.
XX
PE 17-FEB-1998; 98EP-0301169.
XX
PR 29-SEP-1997; 97US-0939300.
PR 19-MAY-1997; 97US-0046957.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Connor JR, James IF, Young PR;
XX
DR WPI: 1998-596881/51.
DR P-PSDB; AAM82543.
XX
PT New IL-1 delta polypeptide and polynucleotide - useful as diagnostic
PT reagents and for diagnosing, prevention or treatment of cancer, AIDS
PT or Alzheimer's disease
XX
PS Disclosure: Page 18-19; 21pp; English.
XX
CC This sequence encodes a novel human interleukin-1 polypeptide, IL-1
CC delta, (interleukin-1 delta) fragment. IL-1 delta polypeptides and
CC polynucleotides are useful for diagnosing susceptibility to diseases
CC by detecting mutations in the IL-1 delta gene. IL-1 delta antibodies
CC are useful for inducing an immune response to immunise and prevent
CC diseases, and for isolating IL-1 delta clones or purifying the
CC polypeptides by affinity chromatography. IL-1 delta polypeptides can

KM	Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW	Immunosuppressant; antirheumatic; arthritic; antipsoriatic;
KV	gene mapping; immune system; treatment; inflammatory disease;
KW	autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KX	psoriasis; human; ds.
XX	
OS	Homo sapiens.
XX	
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FT	/note= "Homologous to mouse IL-1 epsilon protein"
FT	variation
FT	replace (35, A)
FT	/*tag= b
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PN	MO20001174-A1.
PD	
XX	02-MAR-2000.
XX	
PF	20-AUG-1999; 99WO-US18771.
XX	
PR	21-AUG-1998; 98US-0097413.
PR	31-AUG-1998; 98US-0098595.
PR	11-SEP-1998; 98US-0099974.
XX	
PA	(IMMV) IMMUNEX CORP.
PI	
PI	Sims JE, Smith DE;
XX	
DR	WPI: 2000-237653/20.
DR	P-PsDB; MAY70218.
XX	
PT	Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT	treat inflammatory and immune system-related diseases such as
PT	rheumatoid arthritis and inflammatory bowel disease -
XX	
PS	Claim 1a; Fig 1; 76pp; English.
XX	
CC	The present sequence is the polymorphic human Interleukin-1 (IL-1)
CC	epsilon DNA. This gene is mapped to chromosome 2q and is mainly
CC	expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC	tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC	immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC	activity. The DNA sequence can be used in chromosome identification,
CC	gene mapping and study of immune system. IL-1 epsilon can be used in
CC	treatment of inflammatory or autoimmune diseases such as rheumatoid
CC	arthritis, inflammatory bowel disease and psoriasis.
XX	
SO	Sequence 477 BP; 123 A; 123 C; 118 G; 113 T; 0 other;

Query Match 10.8%; Score 134.2; DB 21; Length 477;
 Best Local Similarity 56.8%; Pred. No. 2,4e-30;
 Matches 247; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

OY	340	atctgtgattccgcagacatgtgtgggtcccgagtgaattctttaagcactcct	399
Db	43	atccaggatacatacatcgcgtgggtgtcttcacgaccagaagcgtctaagcaagcccg	102
OY	400	cttaagccgagcatataagccttcaactcttcatttaaatagaccttgtagagacaacaatlc	459
Db	103	aggaagagaccgatgtcttcacgtcacacttatgcttcaatctcatgcgacatgtggagacc	162
OY	460	agtgaagaagaaagggtatatgtttaccctcgggaatcaaggaagaagaatctctgtcc	519
Db	163	cttgaagaagaagaaagggaaccaccaactcaccggtggcctgaatggaatcaatcctgcgcg	222
OY	520	tctctgtgcagaaatccaaggtcaagaccttaactttgcagcttaaggaagaanaataatcatgcag	579
Db	223	atgttgtcctaaagtctggggacacgccccaacgcagctgtgaagaaagaatataataggt	282
OY	580	ctgtatgtgtgagaagaagacagaagaccttctctttccacataaagaagctcc	639

Dd										
Dd	283	tgttacaacccaagcgcgactgttggaagtctcttcctaccacagccagagcgagg	342							
Oy	640	acctctgtctttcaagctctctaccctgctgtgttcatagaacatccacaatca	699							
Dd	343	aactccacctcagactcgttgtcttcccctgctgtgttacgcgtctgaagctcgaaga	402							
Oy	700	ggacaaagccccattcttccaccaagagagagataactaatcaactatcta	759							
Dd	403	ggctgtctccctcattccttaccaccaagaactcggggaagccaactaatgatctgggtta	462							
Oy	760	gattctgttggaataa	774							
Dd	463	actatgctgttttaa	477							
RESULT 9										
ID	AAD06911	standard; cDNA; 819 BP.								
XX	AC									
XX	AA06911;									
DT	03-AUG-2001	(first entry)								
DE	Human interleukin-1 receptor antagonist-like (IL-1ra-L) cDNA.									
KW	Human; interleukin-1 receptor antagonist-like protein; IL-1ra-L; therapy;									
KW	rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;									
KW	joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;									
KW	transplant rejection; graft versus host disease; strain; sprain; leprosy;									
KW	cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;									
KW	clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;									
KW	myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;									
KW	acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;									
KW	eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;									
KW	hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;									
KW	infertility; endometriosis; retinal neuropathy; acute pancreatitis;									
KW	Kawasaki's disease; cancer; ss.									
OS	Homo sapiens.									
FH	Key	Location/Qualifiers								
FT	CDS	1..819								
FT		/*tag= a								
FT		/product= "Human interleukin-1 receptor antagonist-like								
FT		(IL-1ra-L) protein"								
FT		/note= "CDS does not include stop codon"								
FT	/partial									
PN	MO200141792-A1.									
PD	14-JUN-2001.									
PF	04-DEC-2000; 2000MC-US32891.									
PR	10-DEC-1999; 99US-0170105.									
PR	28-NOV-2000; 2000US-0724859.									
PA	(AMGE-) AMGEN INC.									
PI	Calzone FJ, Luethy R, Boedighheimer MJ, Zhu J, Chung Y, Jing S;									
PT	WPI; 2001-381495/40.									
DR	P-SDB; AAE03417.									
XX										
PT	Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the									
PT	polypeptide encoded by the nucleic acid is useful diagnosis, treatment,									
PT	and prevention of diseases such as arthritis, diabetes, transplant									
PT	rejection -									
PS	Claim 1; Fig 1A; 127pp; English.									
XX	The present sequence is human interleukin-1 receptor antagonist-like									

CC (IL-1ra-L) cDNA. IL-1ra-L is useful for treating, preventing or
 CC ameliorating IL-1ra-L polypeptide-related disease, condition or disorder
 CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory
 CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,
 CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft
 CC versus host disease and inflammatory conditions resulting from strain,
 CC sprain, cartilage damage, trauma, orthopedic surgery, hepatitis, human
 CC immunodeficiency virus (HIV) infection, clostridium-associated
 CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,
 CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory
 CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,
 CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,
 CC Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,
 CC lymphomas, lung and breast cancer, leukaemias, infertility,
 CC endometriosis, retinal degeneration, retinal neuropathy, acute
 CC pancreatitis and Kawasaki's disease.

XX Sequence 819 BP; 202 A; 196 C; 204 G; 217 T; 0 other;

Query Match 10.6%; Score 132; DB 22; Length 819;

Best Local Similarity 57.1%; Pred. No. 1.5e-29;
 Matches 240; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 340 attcgtatcttcgcagacagatggtgtgtcctgaagtggaattcttaataagcagctcct 399
 DB 388 attcagatataatcaatcagctggtgtgtcctcagaccagagctcctagagctccg 447
 QY 400 cttagccgacgacatlaagcctgtcactcttcaataagcctgtgagacagaattc 459
 DB 448 aggaagacgctatgtctccagacacactatctcctaattctcctcagacatgtggagacc 507
 QY 460 aggcagaggaagaaaggaatattgttaccctgggaatcaaggaagaagatctctctc 519
 DB 508 ctgagagaagaacagagggagaccacactacactgggacctgaagattcaatccctctg 567
 QY 520 tctctgtcagaactcagggaggaacctcttgcagcttaagaaanaataatcagagac 579
 DB 568 atgtgtctaagtcaggcgaccacccacactgcagctgaagaaagataataatgcat 627
 QY 580 ctgtatgtggaagaagaacagcagacacctctcttccacacataagaagctcc 639
 DB 628 ttgtacaacacacagcagcctgtgaagctctctctcaccacagcagagtgagcag 687
 QY 640 actctgtcttccagatcagctcttaccctgtcgtgttcataagccaccacacatca 699
 DB 688 aactccacctcagctgtgtgtcttccctgtgttcacatcgtcgtcagctcagagga 747
 QY 700 ggaacagccctcttccacacaggaagagacataactaataactacttactta 759
 DB 748 ggcgtctctctcactcctcaccacagaactgggaagcacaactactgacttgggta 807

RESULT 10

ADD12296 standard; DNA; 1073 BP.

AC AAD12296;

DT 16-OCT-2001 (first entry)

XX Human Interleukin-1epsilon (IL-1epsilon) protein DNA.

XX Human; Interleukin-1epsilon; IL-1epsilon; Viruslike; hepatotropic; fever;

KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;

KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;

XX psoriasis; viral infection; allergy; cytokine; HIV; drug screening; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 67..576
 FT CDS /tag= a

FT /product= "Human interleukin-1epsilon (IL-1epsilon)
 FT protein"

XX WO200157219-A2.

XX 09-AUG-2001.

XX 01-FEB-2001; 2001WO-US03285.

XX 02-FEB-2000; 2000US-0179638.

XX (SCHE) SCHERING CORP.

XX Deprets JENA, Timans JC, Bazan JF, Kastelein RA;

XX WPI; 2001-488886/53.

XX P-PSDB; AAE06656.

XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon

XX polypeptide useful for treating conditions exhibiting abnormal

XX expression of interleukin such as immunological disorders, tumor and

XX allergy

XX Claim 18; Page 86-87; 103pp; English.

XX The invention relates to recombinant antigenic interleukin-1 like

XX molecules and their corresponding nucleic acid sequences, designated

XX as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).

XX IL-1delta and IL-1epsilon are useful for treating conditions exhibiting

XX abnormal expression of the interleukin such as immunological disorders,

XX tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,

XX allergy, autoimmune diseases and infectious diseases (e.g., pulmonary

XX tuberculosis, leprosy, fulminant hepatitis, and viral infections such as

XX HIV). The invention also relates to methods of using the composition

XX containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic

XX utilities. IL-1delta is used as an immunogen for the production of

XX antisera or antibodies specific, e.g., capable of distinguishing between

XX IL-1 family members and an IL-1delta, for the interleukin or its

XX fragment. The purified interleukin is used as a reagent to detect any

XX antibodies generated in response to the presence of elevated levels of

XX expression, or immunological disorders which lead to antibody production

XX to the endogenous cytokine. The invention also contemplates the use of

XX competitive drug screening assays. The present DNA sequence encodes human

XX interleukin-1epsilon (IL-1epsilon) protein.

XX Sequence 1073 BP; 281 A; 241 C; 255 G; 296 T; 0 other;

Query Match 10.2%; Score 126.4; DB 22; Length 1073;

Best Local Similarity 56.7%; Pred. No. 8.5e-28;
 Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

QY 338 ctatcgtgatcttcgcagacagatggtgtgtcctgaagtggaattcttaataagcagctc 397
 DB 143 ctatgaatgatttgaatcaagcagatgtgagaccttcaaggtcagacactgtgagctc 202
 QY 398 ctcttagccgacgacatlaagcctgtcactcttcaataagcctgtgagacagaat 457
 DB 203 caggaagtgacagatgtgacccagcagctgtgtgttatcaatcgaagtccagagg 262
 QY 458 tcaatgacaaggaaggaagtaattgttaccctgggaatcaaggaaggaagctctgtc 517
 DB 263 ctcttgagcaagagcagagggagatcccatatttgggaatccagaatccagaatgtgtc 322
 QY 518 tctctgtgcaggaattcagggcagcactcttgaagcttgaaggaanaataatcagtg 577
 DB 323 tgtatgtgagaaggttggagacagccacatltgacgtlaaagaagcagaagatactg 382
 QY 578 accgtatgtgagaagaagacagagaagcctcttcttccacaataaagaagctc 637
 DB 383 atcgtatagcacaacccagcagccgtgaacaccttcttctcagcgtgccaagactgta 442
 QY 638 caactctgtcttctcagtcagctcttaccctgtgctgtgtcatagcactccacacat 697

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Dd 443 ggacctccaccccttgatgctgtgacctcccgacctgcttcatctgctctccaaga--- 499
Oy 698 caggacagcccatcttctcaccagaagagagacataactaactaacttctact 757
Dd 500 gagaccagcccatcttctcactcagacttggagatcatacaacactgcttgaat 559
Oy 758 tagattctgtggaataaataacacagcttag 785
Dd 560 taataataaagtactgaactcagccttag 587

RESULT 11
AAV42659
ID AAV42659 standard; cDNA; 1183 BP.
XX AAV42659;
XX 14-OCT-1998 (first entry)
XX
DE cDNA encoding Interleukin-1 receptor antagonist beta (IL-1ra-beta).
XX
XX Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;
XX IL-1 beta; inflammatory response; treatment; inflammation; septicemia;
XX cancer; anaemia; arthritis; inflammatory bowel disease;
XX graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;
XX acute respiratory disease syndrome; psoriasis; restenosis;
XX traumatic brain injury; acquired immune deficiency syndrome;
XX cachexia; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 75..584
XX FT /tag= a
XX FT /product= IL-1ra-beta
XX
XX EP855404-A1.
XX
XX 29-JUL-1998.
XX
XX 27-JAN-1998; 98EP-0300572.
XX
XX 28-JAN-1997; 97US-0790032.
XX
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX
XX Young PR;
XX
XX WPI: 1998-389778/34.
XX P-PSDB; AAW63136.
XX
XX New nucleic acid encoding human interleukin-1 receptor antagonist
XX beta polypeptides - and related expression systems, transformed
XX cells, proteins, antibodies, agonists and antagonists, useful for
XX treatment, prevention and diagnosis of inflammation, septicemia,
XX cancer etc
XX
XX Claim 3; Fig 1; 20pp; English.
XX
XX The present sequence encodes human Interleukin-1 receptor antagonist
XX beta (IL-1ra-beta). IL-1 alpha and IL-1 beta play key roles in
XX inflammatory responses, and are produced as zymogens which are cleaved
XX upon secretion to yield mature carboxyl terminal 17 KD fragments.
XX IL-1ra-beta polypeptides and polynucleotides are useful in treatment of
XX chronic and acute inflammation, septicemia, cancer, anaemia, arthritis,
XX stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
XX psoriasis, restenosis, traumatic brain injury, acquired immune
XX deficiency syndrome (AIDS) and cachexia. These conditions (or
XX susceptibility to them) may be diagnosed by detecting mutations in the
XX IL-1ra-beta coding sequence analysing a sample for presence or amount
XX of IL-1ra-beta.

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XX
SQ Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;
Query Match 10.2%; Score 126.4; DB 19; Length 1183;
Best Local Similarity 56.7%; Pred. No. 8,9e-28;
Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1;
Oy 338 ctatcgtgattctcgcagatgctgtgctcgtgagttgaattcttaataagagc 397
Dd 151 ctatgaagatttgatcaatcagaagctgtgaccttcaggtcagaacctgtgagcgttc 210
Oy 398 ctctagccgacgacataagcctgtcactcttcaatttaataagcctgtagaacacgaat 457
Dd 211 caggaagtgacagctgtgacctcagctcgtgtgtatcaatgcaagtatccagagg 270
Oy 458 tcaatgacagaagaaaggtaataatggtttacacctgggaatcaagggaagaagatctgtc 517
Dd 271 ctcttgagcaagcgacagagggtatcccatattatttgggaatccagaatccagaatgtgtt 330
Oy 518 tctctgtgacgaataatcagggacagcactcttgacgttaaggaataaataatcatgtg 577
Dd 331 tgtattgtgagaaaggttggagaacagccacattgacgttaaaagcgagaagatcatgtg 390
Oy 578 acctgtatgtggaagaagaagacacagaagcccttctcttccacaataaagaagct 637
Dd 391 atctgtatgccaacccgagcccggtgaaaccttctcttctacgctgccaagactgtgta 450
Oy 638 ccacttctgtcttcaatgactcttaccctgtcgtgttcacgtacacacacacacat 697
Dd 451 ggacctccaccccttgagctgtgacctcccgacctggttcatctgctcccaaga--- 507
Oy 698 caggacagcccatcttctcaccagaagagagacataactaataaactaacttctact 757
Dd 508 gagaccagcccatcttctcactcagacttgggaagtatcatacaacactgcttgaat 567
Oy 758 tagattctgtggaataaataacacagcttag 785
Dd 568 taataataaagtactgaactcagccttag 595

RESULT 12
AAV90135
ID AAV90135 standard; cDNA; 1183 BP.
XX
XX AAV90135;
XX
XX 20-SEP-1999 (first entry)
XX
XX Human Interleukin-1 receptor antagonist beta encoding cDNA.
XX
XX Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;
XX chronic inflammation; acute inflammation; arthritis; autoimmunity;
XX inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;
XX cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;
XX traumatic brain injury; AIDS; cachexia; allergy; parasite infection;
XX allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;
XX allergic inflammatory disease; delayed hypersensitivity; vaccine; ss.
XX
XX Homo sapiens.
XX
XX WO9936541-A1.
XX
XX 22-JUL-1999.
XX
XX 14-JAN-1999; 99WO-US00847.
XX
XX 29-APR-1998; 98US-0069619.
XX 14-JAN-1998; 98US-0007464.
XX
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX
XX Marshall L, Young PR;

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XX WPI: 1999-430615/36.
DR P-PSDB: AAY24395.
XX

PT New interleukin-1 receptor antagonist beta, useful for treating
PT inflammation and autoimmune diseases
XX

PS Claim 5; Fig 1: 34pp; English.
XX

CC The present sequence encodes human interleukin-1 receptor antagonist
CC beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are
CC useful for diagnosing diseases (or susceptibility to diseases) related
CC to the expression or activity of IL-1RA beta, by determining mutations
CC in the IL-1RA beta nucleic acid sequences and/or analysing for the
CC presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides
CC are also useful for screening for compounds which affect activity of the
CC protein. These can be used in treatment to inhibit (antagonist) or
CC enhance (agonist) IL-1RA beta activity, in addition to direct
CC administration of IL-1RA beta polypeptides to treat conditions, or
CC direct administration of antisense sequences to prevent expression.
CC IL-1RA beta polypeptides (administered directly, in a vector i.e. gene
CC therapy, and as a vaccine) and antibodies induce an immune response to
CC include chronic and acute inflammation, diseases diagnosed, prevented or treated
CC inflammatory bowel disease, graft vs. host disease, autoimmunity,
CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,
CC parasite infection, allergic rhinitis, allergic asthma, atopic
CC dermatitis, allergic inflammatory diseases and delayed hypersensitivity.
XX

Sequence 1183 BP: 329 A; 249 C; 269 G; 336 T; 0 other:

Query Match 10.2%; Score 126.4; DB 20; Length 1183;
Best Local Similarity 56.7%; Pred. No. 8.9e-28;
Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

QY 338 ctattcgatcttcgacgaatggtgtggtcgtgagaaatctctaatagacgc 397
DB 151 cctatgaattggaatcagcaagtgtagccctcagagtcagacattgtggaagtc 210
QY 398 ccttagcgcgaacatgaagcctgtcactctccttaataagcctgagacagaat 457
DB 211 caagaaagtacagtgtagcccgctcctgtgtatatacagcaagtcacagaag 270
QY 458 tcaagacagaagaagggtaataatggttaacctgggaatacaaggaagaatctctgtc 517
DB 271 cctctgacagaagcagagggatcccatattgtggatccagatccagaatcgtgt 330
QY 518 tctctgtgacgaattcagagcagcctactcttgcagcttaaggaataaataatcatg 577
DB 331 tgtattgtgagaaggtctgagacaagccatgtagcagcctaagaagagatcatg 390
QY 578 acctgtatgtgagaagaagacagacagcccttctcttccacaataaagaagc 637
DB 391 atctgtatgccaaccgagcccggtgaacacctcttcttaccggtccaagatgta 450
QY 638 ccaactctcttctcagtcagctctcttaacctggtgttcaatagccacctccacacat 697
DB 451 ggaacctccacctgtgctgtgtgcttcccgagctgttcatctgcctccacaaga 507
QY 698 cagagcagccatctcttccacaagagagagacataacataaactactactact 757
DB 508 gagacagccatctcttctcagtaactcagaacttgggaagtcatacaacactgcttgaat 567
QY 758 tagattctgtgaataaataacacgctag 785
DB 568 taatatataatgactgaactcagcctag 595

RESULT 13
AAS26842
ID AAS26842 standard; cDNA: 1183 BP.

XX AAS26842;
AC 07-NOV-2001 (first entry)
XX
DT Human CDNA encoding a novel secreted protein, SEQ ID 34.
XX
DE
DE Human: immunosuppressive; antiarthritic; ss; antirheumatic;
KW cytosolic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW vulnary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
XX
XX WO20015441-A2.
PN
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01320.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225276.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.

Tue May 14 08:26:35 2002

us-09-723-676-1.rng

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2002, 00:03:59 ; Search time 2334.66 Seconds
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Title: us-09-723-676-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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- 29: em.vl:*
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- 31: em.htg.in:*
- 32: em.htg.other:*
- 33: em.htg.in:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description

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	2	690.6	55.5	197308	9	AC016724	Homo sapi
	3	537.4	43.2	585	9	AX052581	Sequence
	4	537.4	43.2	585	9	AF201833	Homo sapi
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	6	329	26.4	1190	6	AX193643	Sequence
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	16	126.4	10.2	1183	9	AF200492	Homo sapi
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	30	70.8	5.7	474	6	AR001464	Sequence
	31	70.8	5.7	474	6	AR055509	Sequence
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	33	70.8	5.7	514	6	AR055509	Sequence
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ALIGNMENTS

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LOCUS	AX167128	Sequence 1 from Patent WO0142305.				
DEFINITION	AX167128					
ACCESSION	AX167128.1	GI:14596616				
VERSION	AX167128.1					
KEYWORDS						
SOURCE						
ORGANISM		human.				
		Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE		1 (bases 1 to 1244)				
AUTHORS		Welcher/A.A., Luethy/R. and Jing,S.				
TITLE		Interleukin-1 receptor antagonist-like molecules and uses thereof				
JOURNAL		Patent: WO 0142305-A 1 14-JUN-2001;				
		Amgen Inc. (US)				
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS AC016724
DEFINITION Homo sapiens BAC clone RP11-339F22 from 2, complete sequence.
ACCESSION AC016724
VERSION AC016724.11 GI:14718389
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 197308)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
9063792
2 (bases 1 to 197308)
Armstrong, J. and Heakenson, W.
The sequence of Homo sapiens BAC clone RP11-339F22
Unpublished (2001)
3 (bases 1 to 197308)
Waterston, R.H.
Direct Submission
Submitted (04-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 197308)
Waterston, R.H.
Direct Submission
Submitted (14-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 197308)
Waterston, R.
Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jul 14, 2001 this sequence version replaced gi:13431151.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0339F22

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NOTICE: This sequence may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-72533; the clone sequenced to the right is RP11-97314. Actual start of this clone is at base position 1 of RP11-339F22; actual end is at base position 197308 of RP11-339F22.

Data from AC084280 and AC024704 was used to finish this clone, AC016724. Polymorphisms have been identified between AC024704 and AC016724.

Sequence derived from PCR from base position 148683 to 149264.

FEATURES

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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Smith,D.E., Renshaw,B.R., Ketchum,R.R., Kubin,M., Garika,K.E. and Sims,J.E.
TITLE Four new members expand the interleukin-1 superfamily
JOURNAL J Biol. Chem. 275 (2), 1169-1175 (2000)
MEDLINE 20092888
REFERENCE 2 (bases 1 to 585)
AUTHORS Sims,J.E.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51 University Street, Seattle, WA 98101, USA
FEATURES
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DB 91 ACAAAGGCTGGAAGACATCATGAGACCAACGAGGAGGACACCCCAATCCTATGCT 150
QY 340 atctgtatcttcgaaagtgtgtgtgtctctgagtgaggaatctttaaagagccct 399
DB 151 ATTCTGATTCGACAGATGCTGTGGTCTGAGTGGAAATCTTTAATAGCAGCTCCT 210
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QY 760 gattctgtggaataa 774
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RESULT 5
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DEFINITION Sequence 9 from Patent WO0140291.
ACCESSION AX193587
VERSION AX193587.1 GI:15211517
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L., Zerhusen,B.D. and Mezes,P.S.
TITLE Proteins and nucleic acids encoding the same
JOURNAL Patent: WO 0140291-A 9 07-JUN-2001; Curagen Corporation (US)
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RESULT 6
LOCUS AX193643 329 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 65 from Patent WO0140291.
ACCESSION AX193643

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VERSION      AX193643.1  GI:15211536
KEYWORDS
SOURCE
ORGANISM     Sus scrofa
              pig.
REFERENCE    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
              1 (bases 1 to 329)
AUTHORS      Burgess, C.E., Prayaga, S.K., Shinkets, R.A., Rastelli, L.,
              Zerhusen, B.D., and Mezes, P.S.
              Proteins and nucleic acids encoding the same
              Patent: WO 0140291-A 65 07-JUN-2001;
              Curagen Corporation (US)
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QY 490 ctgggaatcaaggaagaatctctctctctctgtgcaaaatcagggaacactact 549
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QY 550 ttgcagcttaaggaagaataatcatcagcctgtatgtggaagaagaagaacagagccc 609
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RESULT 7
LOCUS      E28610      1190 bp      DNA      linear      PAT 07-FEB-2001
DEFINITION Novel member of IL-1 family, IL-1-delta.
ACCESSION  E28610
VERSION    E28610.1  GI:13025428
KEYWORDS  JP 1999000177-A/1.
SOURCE    unidentified.
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REFERENCE  1 (bases 1 to 1190)
AUTHORS   Peter, R.Y.I.I. and James, J.R.C.C.
          Novel member of IL-1 family, IL-1-delta
          Patent: JP 1999000177-A 1 06-JAN-1999;
          SMITHKLINE BEECHAM CORP
COMMENT    OS Unidentified
          PN JP 1999000177-A/1
          PD 06-JAN-1999
          PE 16-JAN-1998 JP 1998007091
          PR 19-MAY-1997 US 60/046957, 29-SEP-1997 US 08/939300 PI
          PETER R YOUNG, IAN E JAMES, JANICE R CONNER
          PC C12N15/09, A61K38/00, A61K38/00, A61K38/00, A61K38/00,
          A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K39/395, A61K39/395,
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PC A61K48/00,
PC C07K14/545, C07K16/24, C12P21/02, C12Q1/68, //C12N15/09, C12R1/91,
PC C12N15/00,
PC A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02, A61K37/02,
PC A61K37/02,
PC A61K37/02, A61K37/02, A61K37/02, C12N15/00, C12R1/91 CC
Strandedness: Single;
Topology: Linear;
FH Key Location/Qualifiers
FT source 1..1190
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              1..1190
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Query Match  26.1%; Score 324.4; DB 6; Length 1190;
Best Local Similarity 96.8%; Pred. NO. 1.2e-80;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 220 taactctgtctgttagaacaccagccctccacacatcgtatcttctcttc 279
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QY 280 acaaaagctctgaagacatcatgaaccacaacagggagagcaccaccaatctatgct 339
  -Db 91 ACAAAAGGCTCTGAAAGCATCATGAACCCACAGGGAGGAGCACCACCAATCTATGCT 150
QY 340 atcgtgatctctgacagatggtgtggtcctgtgtgtaaatctttataagactcct 399
  -Db 151 ATTGCTGATTTCTGACAGATGCTGTGGCTCTGATGGAATCTTTATATGACACTCT 210
QY 400 cttagccgcagcatlaagcctgtcactcttcaatlaagcctgtagagacacagaatc 459
  -Db 211 CTTAGCCGCGAGCATTTAGCCTGTGCTCATCTTCAATTAATAGCTGTAGAGACACAATTC 270
QY 460 agtgacagagaagaaggtatattgtttactctgggaatcaaggaagaatctctctc 519
  -Db 271 AGTGACAGAGAAAGGTAATATGTTTACTCTGGGAATCAAGGAAAGATCTGTCTC 330
QY 520 ttctgtgcagaatcagggcagcctactcttgacgttaag 561
  -Db 331 TTCTGTGCAGAATTCAGGGCAAGCTTACTTTGCACTTAAG 372
RESULT 8
LOCUS      E41358      1190 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Novel member of IL-1 family, IL-1delta.
ACCESSION  E41358
VERSION    E41358.1  GI:18625169
KEYWORDS  JP 2000083688-A/1.
SOURCE    unidentified.
          unidentified.
          unclassified.
REFERENCE  1 (bases 1 to 1190)
AUTHORS   Young, P.R., James, I.E. and Conner, J.R.
          Novel member of IL-1 family, IL-1delta
          Patent: JP 2000083688-A 1 28-MAR-2000;
          SMITHKLINE BEECHAM CORP
COMMENT    OS Unidentified
          PN JP 2000083688-A/1
          PD 28-MAR-2000
          PE 01-SEP-1999 JP 1999247635
          PR 19-MAY-1997 US 60/046957, 29-SEP-1997 US 08/939300 PI
          PETER R YOUNG, IAN E JAMES, JANICE R CONNER
          PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K48/00, A61P29/00,
          A61P35/00,
          PC A61P37/02, C07K14/545, C07K16/24, C12N1/15, C12N1/19, C12N1/21, PC
          C12N5/10,

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PC C12P21/02,C12Q1/02,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;

Location/Qualifiers
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BASE COUNT 371 a 227 c 251 g 341 t
ORIGIN

Query Match 26.1%; Score 324.4; DB 6; Length 1190;
Best Local Similarity 96.8%; Pred. No. 1.2e-80;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 220 taactctgctgcttagaaccagcctcctcaaccatctgatactctgtctctc 279
DB 31 TCACCTCTCCTTCACTTTCTTCCAGCCTCCTCACACCATCTGATCTATCTTCTCTTC 90
QY 280 acaaaaggctctgaagacatcatgaaccacaacgggagcgagcaccaccaatctatgct 339
DB 91 ACAAAGGCTCTGAAGACATCATGAACCCACAACGGGAGGACACCCCAATCTATGCT 150
QY 340 attcgtatctcgcagacatggtgtggtcctgagtcggaatcttctaagacgctcct 399
DB 151 ATTCTGATTCCTGACAGATGCTGTGCTCTGATGGAATCTTTAATAGCAGCTCCT 210
QY 400 cttagccgagcatlaagcctctcctcttcaatlaagcctctgtagagacagaattc 459
DB 211 CTTAGCCGAGCATTAAGCCTGTCACTCTTCAATTAACCTGTAGACACAGAAATTC 270
QY 460 agtgaagaagaaagggatataatgattaccctgggaatcaagggaaaagatctctgctc 519
DB 271 ACTGACAAAGAAAGGGATATATGTTTACCTGGGATCAAGGGAAAGATCTCTGTCTC 330
QY 520 ttctgtgcagaattcaaggcaagcctacttgcagcttaag 561
DB 331 TTCTGTGCAGAAATTCAGGGCAAGCCTACTTTCAGCTTAAG 372

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BASE COUNT 371 a 227 c 251 g 341 t
ORIGIN

Query Match 26.1%; Score 324.4; DB 9; Length 1190;
Best Local Similarity 96.8%; Pred. No. 1.2e-80;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 220 taactctgctgcttagaaccagcctcctcaaccatctgatactctgtctctc 279
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QY 280 acaaaaggctctgaagacatcatgaaccacaacgggagcgagcaccaccaatctatgct 339
DB 91 ACAAAGGCTCTGAAGACATCATGAACCCACAACGGGAGGACACCCCAATCTATGCT 150
QY 340 attcgtatctcgcagacatggtgtggtcctgagtcggaatcttctaagacgctcct 399
DB 151 ATTCTGATTCCTGACAGATGCTGTGCTCTGATGGAATCTTTAATAGCAGCTCCT 210
QY 400 cttagccgagcatlaagcctctcctcttcaatlaagcctctgtagagacagaattc 459
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QY 460 agtgaagaagaaagggatataatgattaccctgggaatcaagggaaaagatctctgctc 519
DB 271 ACTGACAAAGAAAGGGATATATGTTTACCTGGGATCAAGGGAAAGATCTCTGTCTC 330
QY 520 ttctgtgcagaattcaaggcaagcctacttgcagcttaag 561
DB 331 TTCTGTGCAGAAATTCAGGGCAAGCCTACTTTCAGCTTAAG 372

RESULT 9
AF200494 1190 bp mRNA linear PRI 11-MAY-2000

LOCUS Homo sapiens interleukin-1 homolog 2 mRNA, complete cds.
DEFINITION AF200494
ACCESSION AF200494
VERSION AF200494.1 GI:7769115

KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1190)
AUTHORS Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,
Griswold,D.E., Capper,E.A., Tal-Singer,R., Wells,G.I., Doyle,M.L.
and Young,P.R.

TITLE Identification and initial characterization of four novel members
of the interleukin-1 family
J. Biol. Chem. 275 (14), 10308-10314 (2000)

JOURNAL MEDLINE 20209405
PUBMED 10744718
2 (bases 1 to 1190)
REFERENCE Kumar,S., McDonnell,P.C. and Young,P.R.
AUTHORS Direct Submission
TITLE Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
Prussia, PA 19406, USA
JOURNAL Location/Qualifiers
1. .1190
/organism="Homo sapiens"
/db_xref="taxon:9606"

FEATURES
source

RESULT 10

E28611 320 bp DNA linear PAT 07-FEB-2001

LOCUS Novel member of IL-1 family, IL-1-delta.
DEFINITION E28611
ACCESSION E28611.1 GI:13025429
VERSION JP 1999000177-A/2.
KEYWORDS unclassified.

SOURCE
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 320)
AUTHORS Peter,R.Y.I.T. and James,J.R.C.C.
TITLE Novel member of IL-1 family, IL-1-delta
Patent: JP 1999000177-A 2 06-JAN-1999;

JOURNAL SMITHKLINE BEECHAM CORP
COMMENT OS Unidentified
PN JP 1999000177-A/2
PD 06-JAN-1999
PE 16-JAN-1998 JP 1998007091
PR 19-MAY-1997 US 60/046957,29-SEP-1997 US 08/939300 PI
PETER R YOUNG, IAN E JAMES, JANICE R CONNER
PC C12N15/09,A61K38/00,A61K38/00,A61K38/00,A61K38/00,
PC A61K38/00
PC A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K39/395,A61K39/395,
PC A61K48/00
PC C07K14/545,C07K16/24,C12P21/02,C12Q1/68/(C12N15/09,C12R1:91),
PC C12N15/00,
PC A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,
PC A61K37/02.

Matches 247; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

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Db 163 CTGGAAGAAGACAGAGAACCCCATCTACCTGGGCTGAATGGACTCATCTCTGCTG 222
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QY 640 acctctgtctcagtcagctctcttacctgtgttcatagaccacctccacacatca 699
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QY 700 ggacagcccatcttctcaccagaagagagacataactaataactactctacta 759
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RESULT 13

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AX207820 1073 bp DNA linear PAT 31-AUG-2001
LOCUS AX207820
DEFINITION Sequence 3 from Patent WO0157219.
ACCESSION AX207820
VERSION AX207820.1 GI:15422467
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1073)
AUTHORS
Debets, J.E., Timans, J.C., Bazan, J.F. and Kastelein, R.A.
TITLE
Mammalian interleukin-1-delta and -epsilon. Their use in
therapeutic and diagnostic methods
Patent: WO 0157219-A 3 09-AUG-2001;
JOURNAL
SCHERING CORPORATION (US)
FEATURES
Source
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BASE COUNT 281 a 241 c 255 g 296 t
ORIGIN

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Query Match 10.2%; Score 126.4; DB 6; Length 1073;
 Best Local Similarity 56.7%; Pred. No. 1.2e-24;
 Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

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Db 203 CACGAAGTGAAGTGTGACCCAGTCACTGTGTGCTTATCATGACATGATTCAGAGG 262
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Db 263 CTCTTGAAGCAAGGAGGATCCATTATTTGTGGAATCAGAAATCCAGAAATGTGTT 322
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Db 560 TAAATATTAATGACTGAACTGACCTAG 587

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RESULT 14

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AF206696 1177 bp mRNA linear PRI 01-NOV-2001
LOCUS AF206696
DEFINITION Homo sapiens interleukin-1 epsilon (IL1E) mRNA, complete cds.
ACCESSION AF206696
VERSION AF206696.1 GI:11493847
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1177)
AUTHORS
Debets, J.E., Timans, J.C., Homey, B., Zurawski, S., Sane, T.R., Lo, S.,
Wagner, J., Edwards, G., Clifford, T., Menon, S., Bazan, J.F. and
Kastelein, R.A.
TITLE
Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,
function as an antagonist and agonist of NF-kappa B activation
through the orphan IL-1 receptor-related protein 2
JOURNAL
J. Immunol. 167 (3), 1440-1446 (2001)
MEDLINE
21359532
PUBMED
11466363

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REFERENCE
2 (bases 1 to 1177)
AUTHORS
Debets, R., Timans, J.C., Zurawski, S., Bazan, J.F. and Kastelein, R.A.
TITLE
Direct Submission
JOURNAL
Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute
of Molecular and Cellular Biology, Inc., 901 California Avenue,
Palo Alto, CA 94304-1104, USA
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BASE COUNT 320 a 249 c 267 g 341 t
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Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

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QY 458 tcagtgacaagaaaggtaataatggttaccctggaatcaaggaaagatctctg 517
DB 263 CTCTTGAGCAAGGACAGAGGGGATCCCATTTATTGGGAATCCAGAAATCCGAAATGTGTT 322
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DB 560 TAAATATTAATGACTGAACTCAGCCTAG 587

RESULT 15
E54910 1183 bp DNA linear PAT 07-FEB-2001
LOCUS Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide.
DEFINITION E54910
ACCESSION E54910.1 GI:13019313
VERSION JP 2000032990-A/1.
KEYWORDS unclassified.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1183)
AUTHORS Peter, R. I.
TITLE Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide
JOURNAL Patent: JP 2000032990-A 1 02-FEB-2000;
SMITHKLINE BEECHAM CORP
OS Unidentified
PN JP 2000032990-A/1
PD 02-FEB-2000
PF 14-MAY-1999 JP 1999134172
PR 28-JAN-1997 US 08/790032
PI PETER R YOUNG
PC C12M15/09, A61K38/00, A61K39/395, A61K45/00, C07K14/545, C07K16/24,

PC C12P21/02,
PC C12O1/02, C12O1/68, G01N33/15, G01N33/50, G01N33/53//A61K31/00, PC
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PC A61K31/00, A61K31/00, C12M15/00, A61K37/02
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1.1183
FT Location/Qualifiers
FT /organism="Unidentified".
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BASE COUNT 329 a 249 c 269 g 336 t
ORIGIN

Query Match 10.2%; Score 126.4; DB 6; Length 1183;
Best Local Similarity 56.7%; Pred. No. 1.2e-24;
Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

QY 338 ctatcgtgattctcgacagatggtggtcctgagtggaattctttaagcagctc 397
DB 151 CTATTAAATGATTGAAATCAGCAAGTGTGACCTTCAGGGTCAGAACCTTGTGGCAGTTT 210
QY 398 ctcttagccgacagcattaaagcctgtactcttcaattaaagcctgtagacacagaat 457
DB 211 CACGAAGTACAGTGTGACCCAGTCACTGTTGCTTATCATCATGCAAGTATCAGAGG 270
QY 458 tcagtgacaagaaaggtaataatggttaccctggaatcaaggaaagatctctg 517
DB 271 CTCTTGAGCAAGGACAGAGGGGATCCCATTTATTGGGAATCCAGAAATCCGAAATGTGTT 330
QY 518 tcttcgtgcaagaattcaaggcaagccttctgcaagcttaagaaataatcatcag 577
DB 331 TGTATTGTGAGAGGTTGGAGAAACGCCACATTTGCACTTAAAGACAGAAATCATGG 390
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DB 451 GGACCTTCACACCTTGAAGTGTGGCCTTCCCGAGCTGTTCAATTCCTCTCCACAGA--- 507
QY 698 caggaagacccatcttctcaccagaagagagcattaactaactaacttact 757
DB 508 GAGACCAAGCCCATCATTTCTGACTTCAGAACTTGGGAAGTACATACACATGCTTTGAAT 567
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DB 568 TAAATATTAATGACTGAACTCAGCCTAG 595

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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1244
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Listing first 45 summaries

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3: em_estlin:*
4: em_estmu:*
5: em_estcov:*
6: em_estcpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	531.2	42.7	870	10	BF244205 601863146
2	286.6	23.0	1219	11	AK009787 Mus muscu
3	284.8	22.9	612	10	BM386666 UT-R-CN1-
4	100.8	8.1	883	11	AK004061 Mus muscu
5	90.6	7.3	475	12	AZ653999 1M0527L24
6	82.2	6.6	536	9	AM853610 RCI-CT025
7	82.2	6.6	559	9	AM578451 RCI-CT025
8	80.6	6.5	539	9	AM368430 CM3-Hr019
9	80.6	6.5	555	9	AM361172 RCI-CT025
10	80.6	6.5	557	10	AM368437 CM3-Hr019
11	79.6	6.4	535	9	BE695960 RCI-CT025
12	79.6	6.4	536	9	AM361164 RCI-CT025
13	73.2	5.9	594	10	BI961215 MONO1_7_E
14	72	5.8	997	9	AL554778 AL554778
15	71.4	5.7	435	10	W78043 zd72d01.r1
16	70.8	5.7	635	9	AM252191 xg62f01.x
17	70.8	5.7	640	10	BG288796 602386126

18	70.8	5.7	864	10	BI489807 603031536
19	70.8	5.7	889	9	AL540334 AL540334
20	70.8	5.7	910	9	AL549965 AL549965
21	70.8	5.7	938	10	BE563703 601335323
22	70.8	5.7	955	10	BM009048 603618892
23	69.2	5.6	549	10	BE706905 QVO-Hr036
24	69	5.5	900	11	AY026753 Homo sapi
25	68.4	5.5	371	10	BI020838 CM4-MT021
26	68.4	5.5	479	9	AA030324 m108c10.r
27	68.4	5.5	1020	10	BG245180 602357579
28	68	5.5	434	9	AM753217 RCI-CT025
29	65.2	5.2	560	9	AM361245 RCI-CT025
30	65.2	5.2	626	9	BB612586 BB612586
31	64.8	5.2	508	9	AM464284 BP230015A
32	60.4	4.9	726	10	BI766516 6030452319
33	59.8	4.8	832	10	BI517352 603041588
34	59.6	4.8	273	10	BI277675 UT-R-C20-
35	57.8	4.6	350	10	BI020732 CM4-MT021
36	57	4.6	281	10	R50241 y158a03.r1
37	56.6	4.5	260	10	R46871 y754f05.r1
38	56.6	4.5	538	9	AM619102 430 MARC
39	55.8	4.5	690	10	BI912302 603069864
40	55.6	4.5	531	9	AM951593 EST36363
41	55.2	4.4	824	10	BI762103 603049281
42	53	4.3	492	9	AM362995 RCI-CT030
43	53	4.3	821	10	BI871339 603592766
44	53	4.3	905	10	BG252897 602365491
45	53	4.3	1051	11	AK009741 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS BF244205 870 bp mRNA linear EST 14-NOV-2000
DEFINITION 601863146p1 NIH-MGC-57 Homo sapiens CDNA clone IMAGE:4080899 5',
mRNA sequence.
ACCESSION BF244205
VERSION BF244205.1 GI:11158135
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
1 (bases 1 to 870)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1995)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLB)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLB at:
http://image.llnl.gov
Plate: LINC941 row: k column: 12
High quality sequence stop: 582.
Location/Qualifiers

FEATURES
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/db_xref="taxon:9606"
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/clone_lib="NIH-MGC-57"
/tissue_type="Glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Brain; Vector: pDNR-LTB (Clontech); Site_1:
sflll (ggcgccctcggcc); Site_2: sflll (ggccatcattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCGCATTTAGCC-3' and 3' adaptor

FEATURES
source
Location/Qualifiers
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putative"

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QTIILTHORGLVNTNFIIESEK"
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polyA_site
/note="putative"
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Best Local Similarity 72.7%; Pred. No. 1.3e-68;
Matches 370; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

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176 ATCTCCAGAAAGTACAGGGTTCTGACTCAGACAGATGATGATGGCTGAGCTGAAA 235
381 tcttcttaataagcgtctcctttagccgcagcagatgaagctctcaattcaatagc 440
236 TACTTAAACGAGCTTCTGCTCTGATGCAACATGTCAGCCTGTCATTTTACTTGATGAC 295
441 ctgtagagacagaatctcgtatgtaattcgtgtaattcgtgtaattcgtgtaattcgt 500
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356 GAAACAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 415
561 gggaaaataataatcgtatgtaattcgtgtaattcgtgtaattcgtgtaattcgtgtaatt 620
416 GGAAGTAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
621 ccaacaataagagcgtccactctgctctctgtaagaaatcagggcaagcctactctgagct 680
476 TCAATGATAGAGGGCTCCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535
681 agcaccacaatcgtatgtaattcgtgtaattcgtgtaattcgtgtaattcgtgtaattcgt 740
536 AGCACCCTCTTCATAGAAAGACAGACATCATCTCTCACATCAGCGGGTAATTTGGT 595
741 taacacaaactctactagatctctgtaagaaatcagggcaagcctactctgagctgagc 800
596 TAAACACTACTTCTACATAGAGCTCTGAGAAATCAATCAATGATGATGATGATGATGATGAT 655
801 ttccagatagagatcaagctgacag 829
656 CTCACGGCCACAGATCAACTGTTGAAG 684

RESULT 3
BM386666/c
LOCUS
DEFINITION
BM386666
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
612 bp mRNA linear EST 17-JAN-2002
UI-R-CNI-cjg-1-09-0-UI-s1 UI-R-CNI Rattus norvegicus cDNA clone
UI-R-CNI-cjg-1-09-0-UI 3', mRNA sequence.
BM386666
BM386666
BM386666.1 GI:18186719
EST.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 612)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704447
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.iowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized fundus library cDNA library Preparation: M.B. Soares Lab
Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 forward
PolyA-Tes.

FEATURES
source

Location/Qualifiers
1..612
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CNI-cjg-1-09-0-UI"
/clone_lib="UI-R-CNI"
/dev_stage="adult"
/lab_host="PH10B (Life Technologies)"
/note="Vector: pT7AD-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CNI
library is a subtracted library derived from the following
pool of seven normalized rat libraries: normalized rat
seminal vesicles, normalized rat penis, normalized rat
bladder, normalized rat cervix, normalized rat brown
adipose, normalized rat fundus, and normalized rat
salivary gland. It was constructed according to the
procedure described by Bonaldo, Lennon & Soares (Genome
Research Genome 6: 791-806, 1996). For construction of
the CNI library, plasmid DNA from the pool of normalized
libraries was electroporated into competent bacteria for
the production of single-stranded circular DNA. This was
then used as a tracer in a subtractive hybridization with
a driver (PCR amplified inserts from a plasmid DNA template
preparation) comprising: a) a pool of about 34,000 clones
from the Rat Urogen Set corresponding to plates R-5-AN-NM
excluding plates R-5-NM and MN. This pool represented 40%
of the final driver population. b) a pool of about 29,000
clones from subtracted libraries CA0 and CA1 corresponding
to plates R-CA0-AMV through R-CA0-AXS, R-CA0-AXZ through
R-CA0-BAX, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS,
R-CA0-BKE, R-CA0-BKG-H, R-CA0-BK-K, R-CA0-BKP through
R-CA0-BKS, R-CA0-BKV-V, R-CA0-BLY through R-CA0-BMA,
R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through
R-CA0-BOJ, R-CA0-BPA through R-CA0-BUF, R-CA1-BBA through
R-CA1-BDA, R-CA1-BHZ through R-CA1-BUF, R-CA1-BUR,

Location/Qualifiers

IMAGE Consortium (info@image.llnl.gov) for further information.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2002, 23:38:04 : Search time 66.4 Seconds
(Without alignments)
4601.929 Million cell updates/sec

Title: US-09-723-676-1

Perfect score: 1244
Sequence: 1 gttgtctccactgctacgtc.....gcatgtcttcttaacctaa 1244

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	324.4	26.1	1190	2	US-08-939-300-1
2	251.8	20.2	320	2	US-08-939-300-3
3	126.4	10.2	1183	2	US-08-790-032-1
4	126.4	10.2	1183	3	US-09-069-619-1
5	70.8	5.7	462	3	US-08-798-414-1
6	70.8	5.7	462	4	US-09-131-247-1
7	70.8	5.7	474	1	US-08-476-860-9
8	70.8	5.7	474	2	US-08-910-733-9
9	70.8	5.7	474	1	US-08-910-884-9
10	70.8	5.7	514	2	US-08-284-784-41
11	70.8	5.7	514	2	US-08-854-811-41
12	70.8	5.7	531	2	US-08-809-185-1
13	70.8	5.7	534	3	US-09-000-630C-24
14	70.8	5.7	534	3	US-08-862-730C-24
15	70.8	5.7	543	3	US-08-422-655-1
16	70.8	5.7	579	2	US-08-476-860-12
17	70.8	5.7	579	2	US-08-910-733-12
18	70.8	5.7	579	2	US-08-910-884-12
19	70.8	5.7	602	1	US-08-459-811-1
20	70.8	5.7	602	1	US-08-459-092-1
21	70.8	5.7	602	2	US-08-459-814-1
22	70.8	5.7	602	2	US-08-425-232-1
23	70.8	5.7	602	2	US-08-471-227-2
24	70.8	5.7	603	1	US-08-484-598-1
25	70.8	5.7	603	2	US-08-479-140-1
26	70.8	5.7	603	3	US-08-477-143-1
27	70.8	5.7	717	1	US-08-284-784-40

28	70.8	5.7	717	2	US-08-854-811-40	Sequence 40, Appl
29	69.2	5.6	1710	3	US-09-000-630C-1	Sequence 1, Appl
30	69.2	5.6	1710	3	US-08-862-730C-1	Sequence 1, Appl
31	69	5.5	998	4	US-09-316-081-1	Sequence 1, Appl
32	69	5.5	998	4	US-09-316-081-1	Sequence 3, Appl
33	68.4	5.5	537	3	US-09-000-630C-25	Sequence 25, Appl
34	68.4	5.5	537	3	US-08-862-730C-25	Sequence 25, Appl
35	68.4	5.5	746	4	US-09-013-810-1	Sequence 1, Appl
36	67	5.4	243	4	US-09-013-810-4	Sequence 4, Appl
37	67	5.4	294	4	US-09-013-810-3	Sequence 3, Appl
38	63.4	5.1	7218	1	US-08-232-463-14	Sequence 14, Appl
39	62.8	5.0	534	3	US-09-000-630C-26	Sequence 26, Appl
40	62.8	5.0	534	3	US-08-862-730C-26	Sequence 26, Appl
41	61.4	4.9	537	3	US-09-000-630C-27	Sequence 27, Appl
42	61.4	4.9	537	3	US-08-862-730C-27	Sequence 27, Appl
43	55.6	4.5	475	4	US-09-131-247-3	Sequence 3, Appl
44	55.6	4.5	1167	4	US-09-131-247-15	Sequence 15, Appl
45	55.6	4.5	1170	4	US-09-131-247-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-939-300-1

Sequence 1, Application US/08939300

Patent No. 5945310

GENERAL INFORMATION:

APPLICANT: Young, Peter R.

APPLICANT: James, Ian E.

TITLE OF INVENTION: A No. 5945310el Member of the IL-1

TITLE OF INVENTION: Family, IL-1 Delta

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAIMER & PRESTITA

STREET: P.O. BOX 980

CITY: VALLEY FORGE

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,300

FILING DATE: 29-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,957

FILING DATE: May 19, 1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTITA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-70018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701

TELEX: 846169

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1190 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-939-300-1

Query Match

Best Local Similarity

26.1%; Score 324.4; DB 2; Length 1190;

96.8%; Pred. No. 1.3e-96;


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Query Match      10.2% Score 126.4; DB 2; Length 1183;
Best Local Similarity 56.7%; Pred. No. 1.9e-31;
Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1.

QY 338 ctatcgcatcttcgcagaatgtygttgctcagtggaattcttbaataagcgtc 397
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Db 151 CTATTAAATGATTTGGAAATCAGCAAGGTGTGACCTTCAGGGTCCAGAACCCTTGCGCAGTTC 210

QY 398 cttctagccgcagcattaaagctgtcacctcttcaattatagcctgttagacacaagaat 457
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 211 CACGAAGGACAGTGTGACCCCGAGTACTGTTGCTGTTATCACATGCAGTAGTATCCAGAG 270

QY 458 tcaagtgaacaagaaaaggtaataatgattactggtgaatcaaggaaaagaatctctgtc 517
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 271 CTCCTGACCAGGAGGAGGAGGATGCCCATTTATTTGGGAATCCAGAAATCCAGAAATGTCTT 330

QY 518 tctctgtgcagaaatltaaggcaagacctactcttgcaagctaagaaaaaatataatctg 577
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 331 TGTATTGTGAGAAAGTTGTGAGAACGCCCACTTTCACAGCTAAAGGCGAAGATATATG 390

QY 578 accttatgtgtagaagaagaacagaaagcccttctctcttccacaataaagaagct 637
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Db 391 ATCTGTATGCCCCAACCCGAGCCCGTGAACCTTCTTTCTTAACCGTCGCMAAGACTGTGA 450

QY 638 ccactctgtcttcaagtcagtcactcttaacctgtgctggtcataagccaactccaccacat 697
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 451 GGACCTCCACCCCTTAGTGTGTGGCTTCCCAGACGTGTTCAATGGCTCTCCACAAA--- 507

QY 698 caggacagcccacttcttcaccaaggagaagggcgaactaactaactaactaacttact 757
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 508 GAGACCAAGCCCACTTCTGACTTCAGAACCTTGGAAGTATACATACACTGCTTGGTGAAT 567

QY 758 tagattctgtggaataaacccagcctag 785
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 568 TAAATATAATGACTGAAGCTCAGCCTAG 595

RESULT 4
US-09-069-619-1
; Sequence 1, Application US/09069619
; Patent No. 6054559
GENERAL INFORMATION:
APPLICANT: Young, Peter and Lisa Marshall
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
TITLE OF INVENTION: Beta (IL-IRA_)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,619
FILING DATE: Herewith
CLASSIFICATION:
Prior Application Data:
APPLICATION NUMBER: 09/007,464; and 08/790,032
FILING DATE: filed 14-JAN-1998; and 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William, T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50051-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:

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? INFORMATION FOR SEQ ID NO: 1:
?   SEQUENCE CHARACTERISTICS:
?       LENGTH: 1183 base pairs
?       TYPE: nucleic acid
?       STRADEDNESS: single
?       TOPOLOGY: linear
?   MOLECULE TYPE: cDNA
?   US-09-069-619-1

Query Match      10.2%; Score 126.4; DB 3; Length 1183;
Best Local Similarity 56.7%; Pred. No. 1.9e-31;
Matches 254; Conservative 0; Mismatches 191; Indels 3; Gaps 1

OY 338 ctatcgcgtatctctcgaacatggtggtggtcctgaatggaattcttaataagcagctc 397
    151 CATTAATGATGATTGGAATCAGCAAGTGWAGACCCCTTCAGGGTCAGAACTTGTGGCAGTTG 210
OY 338 ctatcgcgtatctctcgaacatggtggtggtcctgaatggaattcttaataagcagctc 397
    151 CATTAATGATGATTGGAATCAGCAAGTGWAGACCCCTTCAGGGTCAGAACTTGTGGCAGTTG 210
Db 151 CATTAATGATGATTGGAATCAGCAAGTGWAGACCCCTTCAGGGTCAGAACTTGTGGCAGTTG 210
OY 338 ctatcgcgtatctctcgaacatggtggtggtcctgaatggaattcttaataagcagctc 397
    151 CATTAATGATGATTGGAATCAGCAAGTGWAGACCCCTTCAGGGTCAGAACTTGTGGCAGTTG 210
Db 211 CACGAAAGTGACAGTGAGACCCCAAGTACAGTGTGCTGTATCAGATCCAAAGTATCCAGAG 270
OY 458 tcaagtcacaagaagaaaggtaataatggttacccttggaataccaaggaagaagatcctgtc 517
    271 CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTGGGATTCAGATCCAGAAATGTGTT 330
Db 271 CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTGGGATTCAGATCCAGAAATGTGTT 330
OY 518 tctctcgtcagaatctcaggcgaagcctactcttcagcttgaagaaaaataataatg 577
    331 TGTATGTGAGAAAGGTTGAGAAACGCCCAATTCGACGTAAAGAGCAGAAATGATG 390
OY 578 acctgatctggaagaagaagacagaagccctctctcttcttccaacaataaagaagct 637
    391 ATCTGATGAGCCCAACCCCGAGCCCGTAAACCTTCTTCTACCTGCGCAACAGTGTG 450
Db 391 ATCTGATGAGCCCAACCCCGAGCCCGTAAACCTTCTTCTACCTGCGCAACAGTGTG 450
OY 638 caactctgtcttcacagtcagctcttaccctggtcgtgtcatagcacaacctcacaacat 697
    451 GGACCTCCACCCCTTGAGTGTGTGGCTTCGCCGAGCTGTTCATTTGCTCTCCACAG 507
Db 451 GGACCTCCACCCCTTGAGTGTGTGGCTTCGCCGAGCTGTTCATTTGCTCTCCACAG 507
OY 698 caggaaagcccatctctccaccaagagagagcgaataacataacactacttact 757
    508 GAGACACGACCCATCTTGACTTCAGAACTTGGAAGTATATCAACACTGCTTTGAAT 567
Db 508 GAGACACGACCCATCTTGACTTCAGAACTTGGAAGTATATCAACACTGCTTTGAAT 567
OY 758 tagatctgtggaataatccagcctag 785
    568 TAATATTAATGACTGACTCAGCCTAG 595
Db 568 TAATATTAATGACTGACTCAGCCTAG 595

RESULT 5
US-08-798-414-1
; Sequence 1, Application US/08798414
; Patent No. 6096728
; GENERAL INFORMATION:
;   APPLICANT: COLLINS, David S.
;   TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING
;   TITLE OF INVENTION: INFLAMMATORY DISEASES
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: AMGEN INC.
;   STREET: 1840 De Havilland Drive
;   CITY: Thousand Oaks
;   STATE: California
;   COUNTRY: US
;   ZIP: 91320-1789
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/798,414
;   FILING DATE: 07-FEB-1997
;   CLASSIFICATION: 514

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,419
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,789
FILING DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (Atty Dkt# A-365B-P)
FILING DATE: 23-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ZINDRICK, Thomas D.
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: A-365C
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..462
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..3
OTHER INFORMATION: /note="Initial methionine is
OTHER INFORMATION: optional."
US-08-798-414-1

```

```

Query Match          5 7%; Score 70.8; DB 3; Length 462;
Best Local Similarity 55.2%; Pred. No. 2e-13;
Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```

```

QY 473 aggttaatatgtttactctggaatcaaggaaagatctctctctgtgcagaa 532
|| || || || || || || || || || || || || || || || || || || ||
DB 158 ACCGTCATGCTGCTGTTGGGATCCATGAGGAGATGCTGCTGCTGCTGCTGCT 217
|| || || || || || || || || || || || || || || || || || || ||
QY 533 ttcaggcaagcctacttgcagcttaagaaataatcatcagacctgtatgtgaga 592
|| || || || || || || || || || || || || || || || || || || ||
DB 218 CTGGTGATGAGACCAACATCCAGCTGAGCGCAGTTACATCAGCTGAGCGAGACA 277
|| || || || || || || || || || || || || || || || || || || ||
QY 593 agaagcacagagcctctctctttccacaataaagaagctcactctgtcttc 652
|| || || || || || || || || || || || || || || || || || || ||
DB 278 GAAACGACAGACAGCGCTTCGCTTATCCGCTCAGACAGTGGCCCAACAGTTTG 337
|| || || || || || || || || || || || || || || || || || || ||
QY 653 agtcaagctcttaacctgtgtgtatagcacactccacacatcaggagacccatct 712
|| || || || || || || || || || || || || || || || || || || ||
DB 338 AGTCGCGCGCCCTGCGCGGTGTGCTCTCTGACAGCGATGAGAGTGCAGCCGCTCA 397
|| || || || || || || || || || || || || || || || || || || ||
QY 713 tttccaccaa 722
|| || || || || || || || || || || || || || || || || || || ||
DB 398 GCCTCACCAA 407

```

```

RESULT 6
US-09-131-247-1
; Sequence 1, Application US/09131247
; Patent No. 6294170
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Herhenson, Susan
; APPLICANT: Bevilacqua, Michael P.
; APPLICANT: Collins, David S.
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
; FILE REFERENCE: A-365F
; CURRENT APPLICATION NUMBER: US/09/131,247
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/055,185
; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: PCT/US 97/02131

```

```

; EARLIER FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(462)
; OTHER INFORMATION: Initial methionine is optional
US-09-131-247-1

```

```

Query Match          5 7%; Score 70.8; DB 4; Length 462;
Best Local Similarity 55.2%; Pred. No. 2e-13;
Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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```

QY 473 aggttaatatgtttactctggaatcaaggaaagatctctctctgtgcagaa 532
|| || || || || || || || || || || || || || || || || || || ||
DB 158 agctcatgctctgttcttggaatccatgagggagagatgtgctgtctgtcaagt 217
|| || || || || || || || || || || || || || || || || || || ||
QY 533 ttcaggcaagcctacttgcagcttaagaaataatcatcagacctgtatgtgaga 592
|| || || || || || || || || || || || || || || || || || || ||
DB 218 ctggtgatgagcagactcagctgagggcagttacatcactcagctgagcagaa 277
|| || || || || || || || || || || || || || || || || || || ||
QY 593 agaagcacagagcctctctctttccacaataaagaagctcactctgtcttc 652
|| || || || || || || || || || || || || || || || || || || ||
DB 278 gaaagcaggaacagccttgcccttcacccctcagacagtgagccacacagatttg 337
|| || || || || || || || || || || || || || || || || || || ||
QY 653 agtcaagctcttaacctgtgtgtatagcacactccacacatcaggagacccatct 712
|| || || || || || || || || || || || || || || || || || || ||
DB 338 agtgcgcgcctgcccgcgtgtgttctctctgacacagcagtgagagtgacagccgtca 397
|| || || || || || || || || || || || || || || || || || || ||
QY 713 tttccaccaa 722
|| || || || || || || || || || || || || || || || || || || ||
DB 398 gcttcaccaa 407

```

```

RESULT 7
US-08-476-860-9
; Sequence 9, Application US/08476860
; Patent No. 5739282
; GENERAL INFORMATION:
; APPLICANT: COLOTIA, Francesco
; APPLICANT: MUJOTA, Maria
; APPLICANT: MANTOVANI, Alberto
; TITLE OF INVENTION: IL-1 ANTAGONIST
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,860
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT MI 94 A 002097
; FILING DATE: 13-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: COLOTIA-1
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
FEATURE:
OTHER INFORMATION: Common IL-1ra sequence; a nucleotide G
OTHER INFORMATION: was added in the first position, for computer program
OTHER INFORMATION: reason, in order to encode the first amino acid Glu
OTHER INFORMATION: and further in order to avoid the creation of a stop
OTHER INFORMATION: codon in the inner region of the sequence
FEATURE:
NAME/KEY: CDS
LOCATION: 1..468
US-08-476-860-9

Query Match 5.7%; Score 70.8; DB 1; Length 474;
Best Local Similarity 55.2%; Pred. No. 2e-13;
Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 473 agggtaataatgttaccctgggaataaaggaaagatctctctctctctctctcaga 532
DB 167 agcctatcagt 226
QY 533 ttcagggaagcctactcttgcaacttaagaaaaaatatcatgagcctgtaatgaga 592
DB 227 ctgctgatgagac 286
QY 593 agaaagacacagaagccctctctctctctctctctctctctctctctctctctc 652
DB 287 gaagacagacagac 346
QY 653 agtcaatc 712
DB 347 agctctccgcctc 406
QY 713 ttctcaccaa 722
DB 407 gcctcaccaa 416

RESULT 8
US-08-910-733-9
Sequence 9, Application US/08910733
Patent No. 5837495
GENERAL INFORMATION:
APPLICANT: COLOTTA, Francesco
APPLICANT: MUZIO, Marta
APPLICANT: MANTOVANI, Alberto
TITLE OF INVENTION: INTERLEUKIN-1 ANTAGONIST, DNA ENCODING SAME,
TITLE OF INVENTION: AND ANTIBODIES THEREO
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910.733

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/476,860
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT MI 94 A.002097
FILING DATE: 13-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: COLOTTA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
FEATURE:
OTHER INFORMATION: Common IL-1ra sequence; a nucleotide G
OTHER INFORMATION: was added in the first position, for computer program
OTHER INFORMATION: reason, in order to encode the first amino acid Glu
OTHER INFORMATION: and further in order to avoid the creation of a stop
OTHER INFORMATION: codon in the inner region of the sequence
FEATURE:
NAME/KEY: CDS
LOCATION: 1..468
US-08-910-733-9

Query Match 5.7%; Score 70.8; DB 2; Length 474;
Best Local Similarity 55.2%; Pred. No. 2e-13;
Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 473 agggtaataatgttaccctgggaataaaggaaagatctctctctctctctctcaga 532
DB 167 agcctatcagt 226
QY 533 ttcagggaagcctactcttgcaacttaagaaaaaatatcatgagcctgtaatgaga 592
DB 227 ctgctgatgagac 286
QY 593 agaaagacacagaagccctctctctctctctctctctctctctctctctctctc 652
DB 287 gaagacagacagac 346
QY 653 agtcaatc 712
DB 347 agctctccgcctc 406
QY 713 ttctcaccaa 722
DB 407 gcctcaccaa 416

RESULT 9
US-08-910-884-9
Sequence 9, Application US/08910884
Patent No. 5981713
GENERAL INFORMATION:
APPLICANT: COLOTTA, Francesco
APPLICANT: MUZIO, Marta
APPLICANT: MANTOVANI, Alberto
TITLE OF INVENTION: INTERLEUKIN-1 ANTAGONIST, DNA ENCODING SAME,
TITLE OF INVENTION: AND ANTIBODIES THEREO
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/910,884
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/476,860
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT MI 94 A 002097
FILING DATE: 13-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: COLOTTA-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
FEATURE:
OTHER INFORMATION: Common II-Ira sequence; a nucleotide G
OTHER INFORMATION: was added in the first position, for computer program
OTHER INFORMATION: reason, in order to encode the first amino acid Glu
OTHER INFORMATION: and further in order to avoid the creation of a stop
OTHER INFORMATION: codon in the inner region of the sequence
FEATURE:
NAME/KEY: CDS
LOCATION: 1..468
US-08-910-884-9

Query Match 5.7%; Score 70.8; DB 2; Length 474;
Best Local Similarity 55.2%; Pred. No. 2e-13;
Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
QY 473 aggttaataatggttactcctggaatcaaggaagaatctctgtctctctgtgcaaga 532
DB 167 AGCCTCATGCTCTGTCTTGGAATCATGAGGAGAGATGCTGCTGTCAAGT 226
QY 533 ttcaggcaagcctactcttcagccttaaggaagaaataatcatgacctgatatgtgaga 592
DB 227 CTGCTGATGAGACCAACATCTCAGCTGAGGCACTTAACATCACTGACCTGAGCGAGACA 286
QY 593 agaagacaggaagcccttctcttcttccacaataaagaagcctcactctgtcttc 652
DB 287 GAAAGCAGGACAAAGCGCTTCGCTTCATCCGCTCAGACAGTGGCCCAACACAGTTTG 346
QY 653 agtcagctcttactcctggtgttcatagaccacctccacacacatcaggaagccatct 712
DB 347 AGTGTGCGCGCTGCGCCGGTTGTTCTCTGTGACACAGGATGAGAGCTGACAGCCCGTCA 406
QY 713 ttctccacaa 722
DB 407 GCTTCACCAA 416
RESULT 10

US-08-284-784-41
Sequence 41 Application US/08284784
Patent No. 5629172
GENERAL INFORMATION:
APPLICANT: MASCARENHAS, DESMOND
APPLICANT: ZHANG, YANG
APPLICANT: OLSON, PAMELA S.
APPLICANT: OLSEN, DAVID R.
APPLICANT: CARRILLO, PEDRO A.
TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
TITLE OF INVENTION: TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER SEQUENCES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,784
FILING DATE: 02-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 22095-20275.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-284-784-41

Query Match 5.7%; Score 70.8; DB 1; Length 514;
Best Local Similarity 52.3%; Pred. No. 2.1e-13;
Matches 181; Conservative 0; Mismatches 162; Indels 3; Gaps 1;
QY 473 aggttaataatggttactcctggaatcaaggaagaatctctgtctctctgtgcaaga 532
DB 158 AGCCTCATGCTCTGTCTTGGAATCATGAGGAGAGATGCTGCTGTCAAGT 217
QY 533 ttcaggcaagcctactcttcagccttaaggaagaaataatcatgacctgatatgtgaga 592
DB 218 CTGCTGATGAGACCAACATCTCAGCTGAGGCACTTAACATCACTGACCTGAGCGAGACA 277
QY 593 agaagacaggaagcccttctcttcttccacaataaagaagcctcactctgtcttc 652
DB 278 GAAAGCAGGACAAAGCGCTTCGCTTCATCCGCTCAGACAGTGGCCCAACACAGTTTG 337
QY 653 agtcagctcttactcctggtgttcatagaccacctccacacacatcaggaagccatct 712
DB 338 AGTGTGCGCGCTGCGCCGGTTGTTCTCTGTGACACAGCATGGAAGCTGACAGCCCGTCA 397
QY 713 ttctccacaaagagagacata---actaataacactaactcttacttagattctgtgg 769
DB 398 GCTTCACCAATATGCTGAGAGAGCGCTCATGATGTCACCAATTTACTTCCAGAGAGAG 457
QY 770 aataaatccagccttagctgt 815
DB 458 AGTAAGTACTTGTCTTAATATGATGACCTAGGCTCCCGGGGCTCGAGTA 503

RESULT 11

US-08-854-811-41

Sequence 41, Application US/08854811
Patent No. 5914254

GENERAL INFORMATION:

APPLICANT: Mascarenhas, Desmond

APPLICANT: Zhang, Yang

APPLICANT: Olson, Pamela S.

APPLICANT: Olsen, David R.

TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES

TITLE OF INVENTION: TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESS: MORRISON & FORSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/854,811

FILING DATE: 12-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284,784

FILING DATE: 02-AUG-1994

APPLICATION NUMBER: 08/100,744

FILING DATE: 02-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Buifinger, Nicholas S

REGISTRATION NUMBER: 39,124

REFERENCE/DOCKET NUMBER: 22095-20275.21

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5600

TELEFAX: 650-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 514 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-854-811-41

Query Match

Best Local Similarity 5.7%; Score 70.8; DB 2; Length 514;

Matches 181; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

Db

473 agggtaataatggttactggaatacaagaagatctctgtctctgtgcaaga 532

Db

158 AGGCTCATGTCTGTCTTGGGATCATGAGGAGATGTCCTGCGTGTCAAGT 217

Db

533 tcaaggagagcctacttgcagcttaagaaataatataatgagcctgtatgtgaga 592

Db

218 CTGCTGATGAGACACGACTCCAGCTGAGCGAGTTAATCATCATGAGCCTGAGCGAGACA 277

Db

593 agaaagacagaagccttctcttccacaataaagaagcctcactctgtcttc 652

Db

278 GAAAGCAGGACAGCGCTGCGCTTCATCGCTGACAGATGCGCCACACCACTTTTG 337

Db

653 agtcagctcttaccctgctggtgtcatagcaccctccaccacatcaagaagccatct 712

Db

338 AGTCTGCCGCTGCGCGGTTGTTCTCTGTCACAGCATGGAAGTGAACGACGCGCGTCA 397

RESULT 12

US-08-809-185-1

Sequence 1, Application US/08609185

Patent No. 5922573

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: IL-1 receptor antagonists with increased

NUMBER OF SEQUENCES: 8

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/809,185

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IT MI 94/A 001916

FILING DATE: 21-SEP-1994

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 531 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 1..531

FEATURE:

NAME/KEY: sig_peptide

LOCATION: 1..75

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 76..531

FEATURE:

NAME/KEY: mutation

LOCATION: replace(346..348, "ggc")

OTHER INFORMATION: /note="ggc is the codon for the preferred

OTHER INFORMATION: Asn -> Arg amino acid substitution at this

OTHER INFORMATION: position."

OTHER INFORMATION: position."

US-08-809-185-1

Query Match

Best Local Similarity 5.7%; Score 70.8; DB 2; Length 531;

Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Db

473 agggtaataatggttactggaatacaagaagatctctgtctctgtgcaaga 532

Db

230 AGGCTCATGTCTGTCTTGGGATCATGAGGAGATGTCCTGCGTGTCAAGT 289


```

1  APPLICANT:  Roessler, Blake J.
2  TITLE OF INVENTION:  ADENOVIRAL-MEDIATED GENE TRANSFER TO
3  TITLE OF INVENTION:  SYNOVIAL CELLS IN VIVO
4  NUMBER OF SEQUENCES:  2
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE:  CAMPBELL AND FLORES
7  STREET:  4370 La Jolla Village Drive, Suite 700
8  CITY:  San Diego
9  STATE:  California
10 COUNTRY:  United States of America
11 ZIP:  92122
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE:  Floppy disk
15 COMPUTER:  IBM PC compatible
16 OPERATING SYSTEM:  PC-DOS/MS-DOS
17 SOFTWARE:  PatentIn Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER:  US/08/422,655
20 FILING DATE:
21 CLASSIFICATION:  514
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER:  US 08/100,646
24 FILING DATE:  30-JUL-1993
25 ATTORNEY/AGENT INFORMATION:
26 NAME:  Campbell, Cathryn A.
27 REGISTRATION NUMBER:  31,815
28 REFERENCE/DOCKET NUMBER:  P-UM 9693
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE:  (619) 535-9001
31 TELEFAX:  (619) 535-8949
32 INFORMATION FOR SEQ ID NO:  1:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH:  543 base pairs
35 TYPE:  nucleic acid
36 STRANDEDNESS:  double
37 TOPOLOGY:  linear
38
39 FEATURE:
40 NAME/KEY:  CDS
41 LOCATION:  1..534
42
43 US-08-422-655-1

```

Query Match	5.7%	Score 70.8	DB 1	Length 543
Best Local Similarity	55.2%	Pred. No. 2,2e+13		
Matches 138	Conservative 0	Mismatches 112	Indels 0	Gaps 0
QY 473	agggtataatggtttacctcgtggaatcaagggaagaagatctgtctctctgtgcagaaa	532		
Db 230	AGGCTCAAGCTCTGTTTGTGGAAATCCATGGGAGGAAATGTGCTGTCTTGTCACAT	289		
QY 533	ttcagggaaagcctactcttcagctcctaagaaaatatcatgagcctgtatgtggaga	592		
Db 290	CTGGATGATGAAACCGAGATCCAGCTGGAGGCGATTAACTACTACCTGACGAGAAACA	349		
QY 593	agaaagcagaaagccctttctctttttccacaataaagaagctccactctgtctctc	652		
Db 350	GAAAGCAGAAACCGCTTCGCTTCATCCCTCAGACATGGGCCCAACACAGATTTCG	409		
QY 653	agtaagtcctctaacctgtcgtgttcataagaccctccacacatcagaaagcccat	712		
Db 410	AGTGTGGCGGCTGGCCCGGTTGTTCCTCTGCACAGCATGGAACCTGACCAAGCCGCTCA	469		
QY 713	ttctccaccaa 722			
Db 470	GCTTCACCAA 479			

Search completed: May 13, 2002, 10:50:58
Job time: 40374 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 09:09:50 ; Search time 23.76 Seconds
(without alignments)
489.457 Million cell updates/sec

Title: US-09-723-676-2

Perfect score: 818
Sequence: 1 MNPQREAPKSPYAIRDSRQW.....FLTKRGITNNNTFLDSVE 157

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
A.Geneseq_1101: *
1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT: *
2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT: *
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11: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT: *
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14: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT: *
15: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT: *
16: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT: *
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19: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT: *
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21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT: *
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	818	100.0	157	22	AAE04299 Human Interleukin-
2	818	100.0	157	22	AAE04299 Human IL-1 eta. H
3	777	95.0	170	22	AAE05000 Human Interleukin-
4	452	55.3	164	19	AAE02542 Human IL-1 delta p
5	385	47.1	158	21	AAE02117 Human Interleukin-
6	384	46.9	158	21	AAE02117 Human Interleukin-
7	379	46.3	273	22	AAE03417 Human Interleukin-
8	345.5	42.2	169	19	AAE03136 Human Interleukin-1 rece
9	345.5	42.2	169	20	AAE04043 A human SPOLL-1 pr
10	345.5	42.2	169	20	AAE04395 Human Interleukin-
11	345.5	42.2	169	22	AAE06656 Human Interleukin-

12	345.5	42.2	169	22	AAE03008 Human IL-1ra prote
13	345	42.2	130	22	AAE05001 Human Interleukin-
14	344.5	42.1	208	20	AAE04044 Human SPOLL-II p
15	293.5	35.9	160	19	AAE06286 Rodent interleukin
16	293.5	35.9	160	20	AAE02409 Amino acid sequenc
17	290	35.5	157	22	AAE06662 Mouse interleukin-
18	271.5	33.2	134	21	AAE06935 Human IL-1 recepto
19	271.5	33.2	134	21	AAE06935 Human IL-1 recepto
20	262	32.0	71	19	AAE02543 Human IL-1 delta p
21	234	28.6	218	21	AAE01884 Primate interleuki
22	229	28.0	163	21	AAE07069 Human IL-1 recepto
23	229	28.0	167	21	AAE06932 Human IL-1 recepto
24	229	28.0	176	22	AAE04081 Human extracellular
25	229	28.0	192	21	AAE05297 Human interleukin-
26	229	28.0	193	21	AAE06934 Processed human IL
27	229	28.0	193	22	AAE07596 Human PRO3435. Ho
28	229	28.0	197	21	AAE09300 Human Interleukin-
29	229	28.0	198	22	AAE05138 Human IL-1 recepto
30	229	28.0	203	21	AAE06933 Human IL-1ra fuse
31	229	28.0	207	21	AAE06938 Human IL-1 recepto
32	229	28.0	218	21	AAE08266 Human interleukin-
33	229	28.0	218	21	AAE06940 Human IL-1 recepto
34	229	28.0	218	21	AAE07027 Human zilla4 prote
35	229	28.0	218	21	AAE07033 Human zilla4-E200K
36	229	28.0	218	21	AAE071084 Human zilla4-E200D
37	229	28.0	218	21	AAE05299 Human interleukin-
38	229	28.0	218	21	AAE091885 Primate interleukin
39	229	28.0	218	22	AAE05136 Human IL-1 related poly
40	229	28.0	218	22	AAE047186 Human zilla4 varia
41	227	27.8	218	21	AAE07031 Human IL-1 recepto
42	201.5	24.6	155	21	AAE092254 Human IL-1 recepto
43	200.5	24.5	154	22	AAE035263 Human Interleukin-IL1 re
44	200.5	24.5	155	20	AAE028408 Human Interleukin-
45	200.5	24.5	155	22	AAE087601 Human PRO3442. Ho

ALIGNMENTS

RESULT 1	AAE04299	standard; Protein: 157 AA.
ID	AAE04299	
AC	AAE04299;	
XX		
DE	04-SEP-2001 (first entry)	
XX		
DE	Human Interleukin-1 Receptor Antagonist-Like (IL-1ra-L).	
XX		
KW	Human; Interleukin-1 Receptor Antagonist-Like; IL-1ra-L; atherosclerosis;	
KW	multiple sclerosis; septic shock; anorexia; psoriasis; osteoporosis;	
KW	emphysema; Alzheimer's disease; gene therapy; transthyretin; vulvovaginitis;	
KW	cytostatic; rheumatoid arthritis; autoimmune disease; diabetes; leprosy;	
KW	pulmonary tuberculosis; septicemia; cachexia; hypoglycemia; lung injury;	
KW	Parkinson's disease; eczema; glomerulonephritis; haemorrhage; ischaemia;	
KW	leukaemia; infertility; inflammatory eye disease; acute pancreatitis;	
KW	fibromyalgia.	
OS	Homo sapiens.	
XX		
PN	WO200142305-A1.	
XX		
PD	14-JUN-2001.	
XX		
PF	28-NOV-2000; 2000MO-US24400.	
XX		
PR	10-DEC-1999; 99US-0170052.	
XX		
PA	28-NOV-2000; 2000US-0170052.	
XX		
PI	(AMGE-) AMGEN INC.	
XX		
XX	Welcher AA, Luetly R, Jing S;	

DR WPI; 2001-417857/44.
DR N-PSDB; AAD08531.

PT Novel interleukin-1 receptor antagonist-like polypeptide, its fragment,
PT variant useful for treating multiple sclerosis, septic shock, anorexia,
PT Alzheimer's disease, emphysema, psoriasis, osteoporosis,
PT atherosclerosis -
XX

PS Claim 14; Fig 1; 133pp; English.

CC The present sequence is human interleukin-1 receptor antagonist-like (IL-
CC 1ra-L) protein encoded by IL-1ra-L cDNA (ATCC Deposit No: PTA-1215). IL-
CC 1ra-L DNA and protein are useful for treating, diagnosing, preventing or
CC ameliorating disorders or conditions involving immune system dysfunction
CC (rheumatoid arthritis, inflammatory arthritis, autoimmune disease,
CC multiple sclerosis, diabetes, transplant rejection), infections (leprosy,
CC viral, bacterial, pulmonary tuberculosis, acute phase response or the
CC liver, septicemia or septic shock), weight disorders (obesity, anorexia,
CC cachexia, hypoglycaemia); neuronal dysfunctions (Alzheimer's disease,
CC Parkinson's disease); lung (acute or chronic lung injury); skin (eczema,
CC psoriasis); kidney (acute and chronic glomerulonephritis); bone
CC (osteoporosis, osteopetrosis); vascular system (hemorrhage, ischaemia,
CC haemorrhagic shock, atherosclerosis, congestive heart failure); tumour
CC cells (leukaemias); reproductive system (infertility); eye (inflammatory
CC eye disease). IL-1ra-L DNA and protein are also useful for treating
CC acute pancreatitis, acute fatigue syndrome or fibromyalgia. IL-1ra-L DNA
CC is useful in gene therapy techniques and chromosome mapping.

XX Sequence 157 AA;

Query Match 100.0%; Score 818; DB 22; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPQREAAKSYAIRDSQMWVYLSGNSLIAPLSRSIKPTVLIHLACRDTESDKEN 60
DB 1 mmpqreaaksyairdsqmwvylsgnsliaaplsrslkptvlhlacrdetsdkekn 60
QY 61 MVLGIGKDLCLFCAEIQGKPTQLKEKNIMDLVEKKAQKPFLEFHNKEGSTSVQSV 120
DB 61 mvyigikgdlclfcaeigkptqlkeknimdlvekkakqpflefnkegstsvqsv 120
QY 121 SYPGWFIATSTTSGQPIFLTKERGITNNNTNYLDSVE 157
DB 121 sypgwfiaatsttsgqpifltkergitnntnfyldsve 157

RESULT 2

ID AAB50444 standard; Protein; 157 AA.

XX AAB50444;

XX 13-MAR-2001 (first entry)

XX Human IL-1 eta.

XX Human; IL-1; interleukin-1; IL-1 eta; immunosuppressive;
XX antiinflammatory; antiarthritic; antipsoriatic; inflammation;
XX autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
XX psoriasis.

XX Homo sapiens.

XX MO200071720-A1.

XX 30-NOV-2000.

XX 25-MAY-2000; 2000WO-US14435.

XX 25-MAY-1999; 99US-0135758.
XX 29-OCT-1999; 99US-0162331.

XX (IMV) IMMUNEX CORP.

XX Stims JE, Renshaw BR;

XX WPI; 2001-032039/04.

XX N-PSDB; AAC90487.

PT Novel interleukin-1 eta polypeptides useful as therapeutic agents for
PT treatment of diseases mediated by polypeptide counter-structure
PT molecules and for identifying inhibitors -
XX

PS Claim 4; Page 5; 45pp; English.

CC The present sequence is an interleukin-1 (IL-1) eta polypeptide.
CC The IL-1 eta polypeptide is useful as a therapeutic agent for the
CC treatment of disease mediated by IL-1 eta polypeptide counter-structure
CC molecules and also for identifying proteins associated with IL-1 eta
CC ligands, to screen for potential inhibitors of activity associated with
CC polypeptide counter-structure molecules and in designing inhibitors.
CC It is used to study cellular processes such as immune regulation, cell
CC proliferation, cell death, cell migration, cell-to-cell interaction and
CC inflammatory responses. IL-1 eta promotes inflammatory responses and is
CC involved in the causation and maintenance of inflammatory and/or
CC autoimmune diseases such as rheumatoid arthritis, inflammatory bowel
CC disease, and psoriasis. IL-1 eta polynucleotides can be used to identify
CC IL-1 eta receptors, to study cell signal transduction and the
CC immune system and to identify genes associated with human conditions
CC such as glaucoma, ectodermal dysplasia, insulin-dependent diabetes
CC mellitus, wrinkly skin syndrome, T-cell leukaemia/lymphoma, and tibial
CC muscular dystrophy.

XX Sequence 157 AA;

Query Match 100.0%; Score 818; DB 22; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPQREAAKSYAIRDSQMWVYLSGNSLIAPLSRSIKPTVLIHLACRDTESDKEN 60
DB 1 mmpqreaaksyairdsqmwvylsgnsliaaplsrslkptvlhlacrdetsdkekn 60
QY 61 MVLGIGKDLCLFCAEIQGKPTQLKEKNIMDLVEKKAQKPFLEFHNKEGSTSVQSV 120
DB 61 mvyigikgdlclfcaeigkptqlkeknimdlvekkakqpflefnkegstsvqsv 120
QY 121 SYPGWFIATSTTSGQPIFLTKERGITNNNTNYLDSVE 157
DB 121 sypgwfiaatsttsgqpifltkergitnntnfyldsve 157

RESULT 3

ID AAB85000 standard; Protein; 170 AA.

XX AAB85000;

XX 06-AUG-2001 (first entry)

XX Human interleukin-1 receptor antagonist (NOVINTRA B) polypeptide.

XX NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
XX gonadotropin-like protein; NOVGOV; interleukin-1; NOVINTRA; human;
XX cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
XX antibacterial; cerebroprotective; antidiabetic; antiarthritic;
XX antiasthmatic; anti allergic.

XX Homo sapiens.

XX MO200140291-A2.

XX 07-JUN-2001.

XX	06-DEC-2000; 2000OMO-US33029.	
XX	06-DEC-1999; 9905-0169056.	
PR	09-DEC-1999; 9905-0169866.	
PR	09-DEC-1999; 9905-0169886.	
PR	10-DEC-1999; 9905-0170252.	
PR	12-JAN-2000; 20000US-0175740.	
PR	05-DEC-2000; 20000US-0170252.	
XX		
XX	(CURA-) CURAGEN CORP.	
PA		
XX	Burgess CE, Prayaga SK, Shinkets RA, Rastelli L, Zehrhusen BD;	
PI	Mezes PS;	
PI	WPI: 2001-374790/39.	
DR	N-PSDB; AAF63869.	
XX		
XX	Novel isolated human transmembrane, neuromedin peptide	
PT	gonadotropin-like protein and interleukin-1 receptor antagonist	
PT	proteins, useful for treating cancer, immune response disorder,	
PT	metabolic function disorders -	
XX		
PS	Claim 1; Fig 12b; 138pp: English.	
XX		
CC	The invention provides novel polypeptides (NOVX) selected from human	
CC	transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),	
CC	gonadotropin-like protein (NOVGON) and two interleukin-1 receptor	
CC	antagonist proteins (NOVINTRA A and B). The invention also provides	
CC	methods in which a NOVX polypeptide, polynucleotide and antibody are	
CC	used in the detection, prevention and treatment of a broad range of	
CC	pathological states. NOVTRAN can be used to treat a cell signaling	
CC	disorder such as cancer, immune response disorder, hematopoietic	
CC	disorder, neurodegenerative disorder. NOVNEUR can be used to treat	
CC	endocrine disorder, muscle disorder, neurologic disorder, cancers of	
CC	central nervous system, breast, colon, ovary, kidney, prostate and	
CC	thyroid. NOVGON can be used to treat reproductive development disorder,	
CC	metabolic function disorder and melanoma. NOVINTRA A and B can be used	
CC	to treat bone metabolism or structure disorder, inflammatory response	
CC	disorder, immune regulation disorder, septic shock, stroke, diabetes,	
CC	arthritis and cancer. The present sequence represents the NOVINTRA B	
CC	polypeptide.	
XX		
SO	Sequence 170 AA;	
XX		
Query Match	95.0%; Score 777; DB 22; Length 170;	
Best Local Similarity	100.0%; Pred. No. 2.3e-78;	
Matches 149; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	9 PKSYAIRSRKQMWVLSGNSLIAPLSSIRKVTIHLIACRRTFSDREKGMVYLGICG 68	
DB	22 PKSYAIRSRQMWVLSGNSLIAPLSSIRKVTIHLIACRRTFSDREKGMVYLGICG 81	
QY	69 KDLGFCFAEIQKPTIQLEKKNIMPLYEKKAKQKPFLEFHNKSGTSYQSVYSGWETA 128	
DB	82 KDLGFCFAEIQKPTIQLEKKNIMPLYEKKAKQKPFLEFHNKSGTSYQSVYSGWETA 141	
QY	129 TSTTSGQPIFLTKERGITNNNFYLDYAE 157	
DB	142 TSTTSGQPIFLTKERGITNNNFYLDYAE 170	
RESULT 4		
AAW82542	standard; Protein: 164 AA.	
XX		
AC	AAW82542;	
XX		
DT	08-FEB-1999 (first entry)	
XX		
DE	Human IL-1 delta protein.	
XX		

KW		Infectious mononucleosis; immunise; vaccine; stroke;
KV		interleukin-1; IL-1 delta; human;diagnosis; autoimmune disease;
KM		innoculate; inflammation; arthritis; septicemia; autoimmune disease;
KN		inflammatory bowel disease; psoriasis; transplant rejection; infection;
KO		graft versus host disease; ischemia; acute respiratory disease syndrome;
KP		restenosis; brain injury; AIDS; bone disease; osteoporosis; cancer;
KQ		lymphoproliferative disorder; arteriosclerosis; Alzheimer's disease;
KR		mapping; linkage.
KS		Homo sapiens.
XN		EPR79689-A2.
PB		25-NOV-1998.
XX		17-FEB-1998; 90EP-0301169.
PF		29-SEP-1997; 97US-0939300.
PP		19-MAY-1997; 97US-0046957.
PA	(SMIK) SWITHLINK BEECAM CORP.	
PI	Connor JR, James IE, Young PR;	
DH	WPJ; 1998-596681/51.	
N-PSTDB:	AAV69326.	
New IL-1 delta polypeptide and poly nucleotide - useful as diagnostic reagents and for diagnosing, prevention or treatment of cancer, AIDS or Alzhemner's disease		
Claim 1; Page 18; 21pp; English.		
This sequence represents a novel human interleukin-1 polypeptide, IL-1 delta, (interleukin-1 delta). IL-1 delta polypeptides and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the IL-1 delta gene. IL-1 delta antibodies are useful for inducing an immune response to immunise and prevent diseases, and for isolating IL-1 delta clones or purifying the polypeptides by affinity chromatography. IL-1 delta polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, prevented or treated include: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases e.g. inflammatory bowel disease, psoriasis, transplant rejection, graft versus host disease, infection, stroke, ischemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases e.g. osteoporosis, cancer e.g. lymphoproliferative disorders, arterosclerosis and Alzheimer's disease. The IL-1 delta polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis.		
Sequence 164 AA:		
Query Match 55.3%; Score 452; DB 19; Length 164; Best Local Similarity 94.6%; Pred. No. 2.7e-42; Matches 88; Conservative 1; Mismatches 4; Indels 0; Gaps 0 1 NMPORRAAKSYAINDSRMWLVLSNSLTAIPASISIRPVTLHTACBDTERSDKEKG 60 1 mmpqreaapksyairdsirmvwvlsnsltaipasirsvtlhtlacrdteisdexgn 60 61 MYVLGIGKGDLCFCAEIQGKPILQLKENIMD 93 : 61 myylgikgykdclcfcaeigskptlqlkigsqd 93 RESULT 5 AAV70217 ID AAV70217 standard; Protein; 158 AA. AC AAV70217; XX DT 06-JUN-2000 (first entry)		

```

XX  Human Interleukin-1 epsilon protein.
DE
XX  Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW  immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW  gene mapping; immune system; treatment; inflammatory disease;
KW  autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW  psoriasis; human.
XX
OS  Homo sapiens.
XX
PN  WO200011174-A1.
XX
PD  02-MAR-2000.
XX
PF  20-AUG-1999; 99WO-US18771.
XX
PR  21-AUG-1998; 98US-0097413.
PR  31-AUG-1998; 98US-0098595.
PR  11-SEP-1998; 98US-0099974.
XX
PA  (IMMV ) IMMUNEX CORP.
XX
PI  Sims JE, Smith DE;
XX
DR  WPI: 2000-237653/20.
DR  N-PSDB; AA251247.
XX
PT  Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT  treat inflammatory and immune system-related diseases such as
PT  rheumatoid arthritis and inflammatory bowel disease -
XX
PS  Claim 1b; Fig 2; 76pp; English.
XX
XX  The present sequence is that of human interleukin-1 (IL-1) epsilon
CC  protein. IL-1 epsilon gene is mapped to chromosome 2q and is mainly
CC  expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC  tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC  immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC  activity. It can be used in the treatment of inflammatory or autoimmune
CC  diseases such as rheumatoid arthritis, inflammatory bowel disease and
CC  psoriasis. The DNA sequence can be used in chromosome identification,
CC  gene mapping and study of immune system.
XX
SQ  Sequence 158 AA:

Query Match          47.1%; Score 385; DB 21; Length 158;
Best Local Similarity 49.0%; Pred. No. 7, 1e-35;
Matches 71; Conservative 29; Mismatches 45; Indels 0; Gaps 0;

QY  9 PKSYAIRDSROMVWVLSGNSLIAPLSRSIKPYTLHLIACRDTFESDKEGMMVYLGIKG 68
   1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  10 ppgsgsqdinhvwlvdqdtllavprkdrmspytlalischvetelekdrgnpylging 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  69 KDLICFCAEIOGKPTLQKEKNIMDLVEYKAKQPFLEFHNKSGSTSVFQSVSPGWFIA 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  70 Inlclmcaakvgdptlqkexkdmdlynpqpevkstflfhsqgsgrnstfesvaipwfla 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  129 TSTTSGOPIFLTKERGITNNNTNFFYL 153
   1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  130 vsseggcpllltqelgkanttfdgl 154
   1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
ID  AAY70218 standard; Protein; 158 AA.
XX
AC  AAY70218;
XX
DT  06-JUN-2000 (first entry)
XX
DE  Human Interleukin-1 epsilon polymorphic variant.

```

```

XX  Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW  immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW  gene mapping; immune system; treatment; inflammatory disease;
KW  autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW  psoriasis; polymorphic variant; human.
XX
OS  Homo sapiens.
XX
PN  WO200011174-A1.
XX
PD  02-MAR-2000.
XX
PF  20-AUG-1999; 99WO-US18771.
XX
PR  21-AUG-1998; 98US-0097413.
PR  31-AUG-1998; 98US-0098595.
PR  11-SEP-1998; 98US-0099974.
XX
PA  (IMMV ) IMMUNEX CORP.
XX
PI  Sims JE, Smith DE;
XX
DR  WPI: 2000-237653/20.
DR  N-PSDB; AA251248.
XX
PT  Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT  treat inflammatory and immune system-related diseases such as
PT  rheumatoid arthritis and inflammatory bowel disease -
XX
PS  Claim 1b; Fig 2; 76pp; English.
XX
XX  The present protein sequence is that of human interleukin-1 (IL-1)
CC  epsilon polymorphic variant. IL-1 epsilon gene is mapped to chromosome 2q
CC  and is mainly expressed in spleen, lymph node, thymus, tonsil and
CC  leucocyte tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC  immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC  activity. It can be used in the treatment of inflammatory or autoimmune
CC  diseases such as rheumatoid arthritis, inflammatory bowel disease and
CC  psoriasis. The DNA sequence can be used in chromosome identification,
CC  gene mapping and study of immune system.
XX
SQ  Sequence 158 AA:

Query Match          46.9%; Score 384; DB 21; Length 158;
Best Local Similarity 49.0%; Pred. No. 9, 1e-35;
Matches 71; Conservative 29; Mismatches 45; Indels 0; Gaps 0;

QY  9 PKSYAIRDSROMVWVLSGNSLIAPLSRSIKPYTLHLIACRDTFESDKEGMMVYLGIKG 68
   1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  10 ppgsgsqdinhvwlvdqdtllavprkdrmspytlalischvetelekdrgnpylging 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  69 KDLICFCAEIOGKPTLQKEKNIMDLVEYKAKQPFLEFHNKSGSTSVFQSVSPGWFIA 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  70 Inlclmcaakvgdptlqkexkdmdlynpqpevkstflfhsqgsgrnstfesvaipwfla 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  129 TSTTSGOPIFLTKERGITNNNTNFFYL 153
   1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  130 vsseggcpllltqelgkanttfdgl 154
   1: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
ID  AAE03417 standard; Protein; 273 AA.
XX
AC  AAE03417;
XX
DT  03-AUG-2001 (first entry)
XX
DE

```

[illegible]

Oy	129	TSTSGOPIFLTKRGITNNNFYL	153
	:	:	:
	:	:	:
	:	:	:
	:	:	:
Db	245	vsseggcplltqelgkxantldtgrl	269
RESULT 8			
	AAW63136		
ID	AAW63136	standard; Protein; 169 AA.	
XX	AAW63136;		
XX			
DE	14-OCT-1998	(first entry)	
XX			
XX	Interleukin-1 receptor antagonist beta (IL-1ra-beta).		
KW	Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;		
KW	IL-1 beta; inflammatory response; treatment; inflammation; septicæmia;		
KW	cancer; anaemia; arthritis; inflammatory bowel disease;		
KW	graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;		
KW	acute respiratory disease syndrome; psoriasis; restenosis;		
KW	traumatic brain injury; acquired immune deficiency syndrome;		
KW	cachexia.		
OS			
XX	Homo sapiens.		
XX			
PN	EP855404-AL.		
PD	29-JUL-1998.		
XX			
PF	27-JAN-1998;	98EP-0300572.	
XX			
PR	28-JAN-1997;	97US-0790032.	
XX			
PA	(SMTK) SMITHKLINE BEECHAM CORP.		
XX			
PI	Young PR;		
XX			
DR	WPI: 1998-389778/34.		
XX			
DR	N-PSDB; AAW42659.		
PT			
XX	New nucleic acid encoding human interleukin-1 receptor antagonist		
PT	beta polypeptides - and related expression systems, transformed		
PT	cells, proteins, antibodies, agonists and antagonists, useful for		
PT	treatment; prevention and diagnosis of inflammation, septicæmia,		
PT	cancer etc		
XX			
PS			
XX	Claim 13; Fig 2; 20pp; English.		
XX			
CC	The present sequence represents human interleukin-1 receptor antagonist		
CC	beta (IL-1ra-beta). IL-1 alpha and IL-1 beta play key roles in		
CC	inflammatory responses, and are produced as zymogens which are cleaved		
CC	upon secretion to yield mature carboxyl terminal 17 kD fragments.		
CC	IL-1ra-beta polypeptides and polynucleotides are useful in treatment of		
CC	chronic and acute inflammation, septicæmia, cancer, anaemia, arthritis,		
CC	inflammatory bowel disease, graft vs. host rejection, autoimmunity,		
CC	stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),		
CC	psoriasis, restenosis, traumatic brain injury, acquired immune		
CC	deficiency syndrome (AIDS) and cachexia. These conditions (or		
CC	susceptibility to them) may be diagnosed by detecting mutations in the		
CC	IL-1ra-beta coding sequence analysing a sample for presence or amount		
CC	of IL-1ra-beta.		
XX			
XX			
SO	Sequence	169 AA;	
Query Match 42.2%; Score 345.5; DB 19; Length 169;			
Best Local Similarity 43.0%; Pred. No. 1.9e-30;			
Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;			
Oy	4	GREAPKSVYIRDSRWVWVLISGNLIAPLSIRSIPTVLHLIACRDTFESDKRGNNMY	63
	:	:	:
	:	:	:
	:	:	:
	:	:	:
Db	17	qsmckphtgclndngvvtlqgnlvavprdsrvptvavlttckypaalqsgtdpdy	76

OY	64	IGFKGDLCEFCALQCKPTLTLEKNNIMDLVYEKKAKPCLFEFNKSESTVSPOVSAP	123
Db	77	LGfqpmeclcyecvgeqgqllqkqkmdlyg9gqpevpkpfllfyakrgtstlesvalp	136
OY	124	GWEIATSTTSGQPIFLTKERGITNNTFEYID	154
Db	137	dwfiaasskrd-qpliltsejgksyntafeln	166
RESULT	9		
ID	AAAY24043	standard; Protein; 169 AA.	
XX	AAAY24043;		
DT	30-SEP-1999	(first entry)	
XX			
DE		A human SPOIL-I protein (also known as hRANGO 080-I).	
XX		SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;	
KW		bone metabolism disorder; proinflammatory disorder; immune disorder;	
KW		inflammatory disease; septic shock; stroke; diabetes; arthritis;	
KW		intercolitis; pneumonitis; epithelial cell; skin disease;	
KW		proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;	
KW		epithelial cancer; squamous cell carcinoma; bone resorption disorder;	
KW		osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;	
KW		osteogenesis imperfecta; fibrous dysplasia; hypophosphatasia;	
KW		bone sarcoma; myeloma bone disorder; osteolytic bone lesion;	
KW		hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;	
KW		bone fracture; hRANGO 80-I.	
XX			
OS		Homo sapiens.	
XX			
PN	W09937662-A1.		
PD	29-JUL-1999.		
XX			
PF	26-JAN-1999;	99WO-US01575.	
XX			
PR	27-JAN-1998;	98US-0013810.	
XX			
PA	(MILL-) MULLENNIUM BIOTHERAPEUTICS INC.		
XX			
PI	Busfield SJ;		
XX			
DR	WPI; 1999-458675/38.		
DR	N-PSDB; AAX86458.		
PT		New isolated SPOIL proteins, used to develop products for treating,	
PT		e.g. inflammatory and immune disorders	
XX			
PS			
XX			
XX		Example 1; Fig 4A-B; 126pp; English.	
CC		The present sequence represents a SPOIL-I protein. SPOIL proteins have	
CC		homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.	
CC		The SPOIL proteins are used as modulating agents in regulating a variety	
CC		of cellular processes. The products can be used for treating disorders	
CC		characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone	
CC		metabolism disorder, a proinflammatory disorder or an immune disorder.	
CC		They can be used for treating e.g. inflammatory diseases and disorders	
CC		e.g. inflammation, septic shock, stroke, diabetes, arthritis,	
CC		intercolitis and pneumonitis, epithelial cell and/or skin diseases and	
CC		disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma	
CC		and Kaposi's sarcoma and other epithelial cancers including squamous cellu	
CC		carcinoma, oesophageal cancer and cancer of the mouth and/or throat), and	
CC		bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's	
CC		disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,	
CC		fibrous dysplasia, hypophosphatasia, bone sarcoma, myeloma bone disorder	
CC		(e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and	
CC		SPOIL modulators are useful for regulation of bone mass (e.g. increase in	
CC		bone mass and/or inhibit bone loss), management of bone fragility (e.g.	
CC		decrease bone fragility); and prevention and/or treatment of bone pain,	

	CC	bone deformities and/or bone fractures. The products can also be used for
	CC	detection, diagnosis and screening assays.
	xx	
SQ	Sequence	169 AA:
Query Match	42.2%; Score 345.5; DB 20;	Length 169;
Best Local Similarity	45.0%; Pred. No. 1.9e-30;	
Matches	68; Conservative	29; Mismatches 53; Indels 1.; Gaps 1
OY	4 OREAPKSVATIRDSROMVVLGSGNSLIAPLSRIKPVTLLIACDTEFSDKEKNMAY	63
	: : : :	
Dd	17 gsmcxfpiybtindlnqvvcltggqnlvayprdsdvrvavalcycypaalvgyrdgdpdy	76
OY	64 LGIKRGDIQLPCAETIQGRPTTLQLEKENIMDLVEYKKAKPFLFFHNHKEGSTVFQSVP	123
	: : : : : : : : : : : : : : : : : :	
Dd	77 lgiqpemciylceakvgcgptlqlkeqkindlysgpeqvvpflfyzakrtgrttlevalcp	136
OY	124 GWFIATSTSGOPIELTKRGTITNNMFPLD	154
	:	
Dd	137 dwfiasskrdd-qpilittselgksyntafeln	166

RESULT 10	
AAV24395	
ID	AAV24395 standard; Protein: 169 AA.
XX	
AC	AAV24395;
XX	
DT	20-SEP-1999 (first entry)
XX	
DE	Human interleukin-1 receptor antagonist beta.
XX	
KW	Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;
KW	chronic inflammation; acute inflammation; arthritis; autoimmunity;
KW	inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;
KW	cardiac ischaemia; acute respiratory disease syndrome; ARDS; resection
KW	traumatic brain injury; AIDS; cachexia; allergy; parasite infection;
KW	allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;
KW	allergic inflammatory disease; delayed hypersensitivity; vaccine.
XX	
OS	Homo sapiens.
XX	
PN	WO936541-A1.
XX	
PD	22-JUL-1999.
XX	
PF	14-JAN-1999; 99WO-0500847.
XX	
PR	29-APR-1998; 98US-0069619.
PR	14-JAN-1998; 98US-0007464.
XX	
PA	(SMK) SMITHKLINE BEECHAM CORP.
XX	
PI	Marshall L, Young PR;
XX	
DR	WPI: 1999-430615/36.
DR	N-PSDB: AAX90135.
XX	
PT	New interleukin-1 receptor antagonist beta, useful for treating
PT	inflammation and autoimmune diseases
XX	
PS	Claim 15; Fig 1; 34pp; English.
XX	
CC	The present sequence represents human interleukin-1 receptor antagonist
CC	beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are
CC	useful for diagnosing diseases (or susceptibility to diseases) related
CC	to the expression or activity of IL-1RA beta, by determining mutations
CC	in the IL-1RA beta nucleic acid sequences and/or analysing for the
CC	presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides
CC	are also useful for screening for compounds which affect activity of the
CC	protein. These can be used in treatment to inhibit (antagonist) or
CC	enhance (agonist) IL-1RA beta activity, in addition to direct

CC molecules and their corresponding nucleic acid sequences, designated
 CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
 CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
 CC abnormal expression of the interleukin such as immunological disorders,
 CC tumors, inflammatory disorders, fever, hypoglycemia, psoriasis,
 CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
 CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
 CC HIV). The invention also relates to methods of using the composition
 CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
 CC utilities. IL-1delta is used as an immunogen for the production of
 CC antisera or antibodies specific, e.g., capable of distinguishing between
 CC IL-1 family members and an IL-1delta, for the interleukin or its
 CC fragment. The purified interleukin is used as a reagent to detect any
 CC antibodies generated in response to the presence of elevated levels of
 CC expression, or immunological disorders which lead to antibody production
 CC to the endogenous cytokine. The invention also contemplates the use of
 CC competitive drug screening assays. The present sequence is human
 CC interleukin-1epsilon (IL-1epsilon) protein.

XX Sequence 169 AA;

Query Match 42.2%; Score 345.5; DB 22; Length 169;

Best Local Similarity 45.0%; Pred. No. 1.9e-30;

Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;

QY 4 QREAPKSYAIRDSROWVWVLSGNSLIAPLSRSIKPVTLLIACRDPFEFSKRNMY 63
 DB 17 gsmckpigtindngqvwlvlggnlvavprsdvtpvtvavickypaalegqrdpily 76
 QY 64 LGIKGKDLCLFCAEIQGKPTLQLEKKNIMDLVEKKAOKPFLFHNKSGTSVFSVSYP 123
 DB 77 LGIQNPemclyckvgeqptlqkqkmdlygqpevpkpflyrktgrtlesvafrp 136
 QY 124 GWFIASTSTSGOPFLFKERGITNTNTNYLD 154
 DB 137 dwfiasskrd-qpiltsejgksyntafeln 166

RESULT 12

AAB83008

AAB83008 standard; protein; 169 AA.

XX AAB83008;

XX 21-JUN-2001 (first entry)

XX Human IL-1ra protein.

XX Human; IL-1ra; interleukin-1 receptor antagonist; antibacterial;
 KW immunosuppressive; antiinflammatory; antiarthritic; nephrotropic;
 KW hepatotropic; virucide; cardiatic; vasotropic; antiidiabetic; cancer;
 KW neuroprotective; osteoprotic; cytotoxic; immunomodulator; nocitropic;
 KW cerebroprotective; antidepressant; antiarteriosclerotic; infection;
 KW immune disease; autoimmune disease; bone disease; neuronal disease;
 KW cardiovascular disease.

XX Homo sapiens.

XX WO200119390-A1.

XX 22-MAR-2001.

XX 28-AUG-2000; 2000WO-TB01192.

XX 14-SEP-1999; 99US-0154010.

XX (PFIZ) PFIZER PROD INC.

XX Liltman BH, Woodworth TLG, Dombroski MA;

XX WPI; 2001-327986/34.

PT Synergistic treatment of interleukin (IL)-mediated diseases, useful for
 PT e.g. septic shock, comprises adjunctively administering IL-1 receptor
 PT antagonist polypeptide and non-steroidal IL-1 processing and release
 PT inhibiting agent.

XX Disclosure; Page 91; 112pp; English.

XX The present sequence is a human interleukin-1 receptor antagonist
 CC (IL-1ra). The present sequence or its variant may be administered
 CC in combination with a non-steroidal IL-1 processing and release
 CC inhibiting agent for the treatment or prevention of IL-mediated disease
 CC states. The composition is useful for treating inappropriate host
 CC responses to infectious diseases where active infection exists at any
 CC body site, e.g. septic shock, disseminated intravascular coagulation,
 CC and/or adult respiratory distress syndrome, acute or chronic
 CC inflammation due to antigen, antibody and/or complement deposition;
 CC inflammatory conditions including arthritis, cholangitis, colitis,
 CC encephalitis, endocarditis, glomerulonephritis, hepatitis, myocarditis,
 CC pancreatitis, pericarditis, and reperfusion injury vasculitis. It is
 CC also useful for treating immune-based diseases including conditions
 CC involving T cells and/or macrophages e.g. acute and delayed
 CC hypersensitivity, graft rejection, graft-versus-host disease;
 CC autoimmune diseases including Type 1 diabetes mellitus and multiple
 CC sclerosis. The composition may be used for treating bone and cartilage
 CC resorption as well as diseases resulting in excess deposition of
 CC extracellular matrix. Such diseases include osteoporosis, periodontal
 CC diseases, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis
 CC and keloid formation. It is also useful for treating tumors which
 CC produce IL-1 as an autocrine growth factor and for preventing the
 CC cachexia associated with certain tumors. It may be used for
 CC treating neuronal diseases with an inflammatory component e.g.
 CC Alzheimer's disease, stroke, depression and concussion injury and for
 CC cardiovascular diseases in which recruitment of monocytes into the
 CC subendothelial space plays a role, e.g. the development of
 CC atherosclerotic plaques.

XX Sequence 169 AA;

Query Match 42.2%; Score 345.5; DB 22; Length 169;

Best Local Similarity 45.0%; Pred. No. 1.9e-30;

Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;

QY 4 QREAPKSYAIRDSROWVWVLSGNSLIAPLSRSIKPVTLLIACRDPFEFSKRNMY 63
 DB 17 gsmckpigtindngqvwlvlggnlvavprsdvtpvtvavickypaalegqrdpily 76
 QY 64 LGIKGKDLCLFCAEIQGKPTLQLEKKNIMDLVEKKAOKPFLFHNKSGTSVFSVSYP 123
 DB 77 LGIQNPemclyckvgeqptlqkqkmdlygqpevpkpflyrktgrtlesvafrp 136
 QY 124 GWFIASTSTSGOPFLFKERGITNTNTNYLD 154
 DB 137 dwfiasskrd-qpiltsejgksyntafeln 166

RESULT 13

AAB85001

AAB85001 standard; protein; 130 AA.

XX AAB85001;

XX 06-AUG-2001 (first entry)

XX Human interleukin-1 receptor antagonist (NOVINTRA C) polypeptide.

XX NOVX; transmembrane protein; NOVTRAN; neuromedine peptide; NOVNEOR;
 KW gonadotropin-like protein; NOVGOIN; interleukin-1; NOVINTRA; human;
 KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
 KW antibacterial; cerebroprotective; antiidiabetic; antiarthritic;
 KW antiasthmatic; antiallergic.

XX Homo sapiens.

XX	W0200140291-A2.
PN	
XX	
PD	07-JUN-2001.
XX	
PF	06-DEC-2000; 2000MO-US33029.
PR	
PR	06-DEC-1999; 99US-0169056.
PR	09-DEC-1999; 99US-0169866.
PR	09-DEC-1999; 99US-0169886.
PR	10-DEC-1999; 99US-0170252.
PR	12-JAN-2000; 2000US-0175740.
PR	05-DEC-2000; 2000US-0170252.
XX	
PA	(CURA-) CURAGEN CORP.
PI	Burgess CE, Prayaga SK, Shinkets RA, Rastelli L, Zernhusen BD;
PI	Mezes PS;
XX	
DR	N-PSDB: AAF83870.
DR	MP1: 2001-374790/39.
XX	
PT	Novel isolated human transmembrane, neuromedin peptide
PT	gonadotropin-like protein and interleukin-1 receptor antagonist
PT	metabolic function disorders - immune response disorder,
XX	
PS	Claim 53; Fig 15B; 138pp; English.
XX	
CC	The invention provides novel polypeptides (NOVA) selected from human
CC	transmembrane protein (NOVTRAP), neuromedin peptide (NOVNEUR),
CC	gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC	antagonist proteins (NOVINTRA A and B). The invention also provides
CC	methods in which a NOVA polypeptide, polynucleotide and antibody are
CC	used in the detection, prevention and treatment of a broad range of
CC	pathological states. NOVTRAN can be used to treat is a cell signaling
CC	disorder such as cancer, immune response disorder, hematopoietic
CC	disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC	endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC	central nervous system, breast, colon, ovary, kidney, prostate and
CC	thyroid. NOVGON can be used to treat reproductive development disorder,
CC	metabolic function disorder and melanoma. NOVINTR A and B can be used
CC	to treat bone metabolism or structure disorder, inflammatory response
CC	disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC	arthritis and cancer. The present sequence represents the NOVINTRA C
CC	polypeptide.
XX	
SQ	Sequence 130 AA;
XX	
Query Match	42.2%; Score 345; DB 22; Length 130;
Best Local Similarity	50.4%; Pred. No. 1.5e-30;
Matches 66; Conservative 25; Mismatches 36; Indels 4; Gaps	
OY	16 DSRQMWVVWSGNSILTAAPLSRSIKVTPLHLICRPTSEFSDKRGMMVYGIKGDLCFC 75 : : : :
Db	1 dlnhvwaVgdqdliaav--ikvfpvtalIschrivetelekrpnipiyigInlclmc 58 : : : :
OY	76 AEIOGKPTLQLK-EKNIMDLVEKKAKOPLFLFHFKEGSTVSFOSVSYGMFIATSTTS 133 : : : : : : :
Db	59 akvgdptqlklgkeldimldynqppepvksflfysgsgrnsttfesvaIfgyfflawssag 118 : : :
OY	134 GGPFIPLTKERG 144
Db	119 gcpllltgelg 129
RESULT 14	
AAV24044	
ID	AAV24044 standard; Protein; 208 AA.
AC	AAV24044;
XX	

PT		30-SEP-1999	(first entry)
XX		A human SPOIL-II protein (also known as hRANGO 080-II).	
DE		SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;	
XX		bone metabolism disorder; proinflammatory disorder; immune disorder;	
KW		Inflammatory disease; septic shock; stroke; diabetes; arthritis;	
KM		intercolitis; pneumonitis; epithelial cell; skin disease;	
KW		Proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;	
KW		epithelial cancer; squamous cell carcinoma; bone resorption disorder;	
KW		osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;	
KW		osteogenesis imperfecta; fibrous dysplasia; hypophosphatemia;	
KW		bone sarcoma; myeloma bone disorder; osteolytic bone lesion;	
KW		hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;	
KW		bone fracture; hRANGO 80-I.	
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	98..724	
FT		/tag= a	
FT		/product= SPOIL-II	
XX			
PN	W09937662-AI.		
PD	29-JUL-1999.		
XX			
PF	26-JAN-1999;	99WO-US01575.	
XX			
PR	27-JAN-1998;	98US-0013810.	
PA	(MILL-) MILLENNIUM BIOTHERAPUTICS INC.		
XX			
PI	Bushfield SJ;		
XX			
DR	WPI: 1999-458675/38.		
DR	N-PSSDI; AAX86459.		
XX			
PT	New isolated SPOIL proteins, used to develop products for treating,		
PT	e.g. inflammatory and immune disorders		
XX			
PS	Claim 8; Fig 5; 126pp; English.		
XX			
CC	The present sequence represents a SPOIL-II protein. SPOIL proteins have		
CC	homology to Interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.		
CC	The SPOIL proteins are used as modulating agents in regulating a variety		
CC	of cellular processes. The products can be used for treating disorders		
CC	characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone		
CC	metabolism disorder, a proinflammatory disorder or an immune disorder.		
CC	They can be used for treating e.g. inflammatory diseases and disorders		
CC	e.g. inflammation, septic shock, stroke, diabetes, arthritis,		
CC	intercolitis and pneumonitis, epithelial cell and/or skin diseases and		
CC	disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma		
CC	and Kaposi's sarcoma and other epithelial cancers including squamous cell		
CC	carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and		
CC	bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's		
CC	disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,		
CC	fibrous dysplasia, hypophosphatemia, bone sarcoma, myeloma bone disorder		
CC	(e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and		
CC	SPOIL modulators are useful for regulation of bone mass (e.g. increase in		
CC	bone mass and/or inhibit bone loss), management of bone fragility (e.g.		
CC	decrease bone fragility); and prevention and/or treatment of bone pain,		
CC	bone deformities and/or bone fractures. The products can also be used for		
CC	detection, diagnosis and screening assays.		
XX			
SQ	Sequence	208 AA;	
	Query Match	42.1%; Score 344.5; DB 20; Length 208;	
	Best Local Similarity	45.9%; Pred. No. 3.2e-30;	
	Matches 67; Conservative 29; Mismatches 49; Indels 1; Gaps 1.		
QY	9 PYSVAIRDSROMWWLGSNSLIAPALSRISIKPYTTLILACRPTEFSDRKGMVYIGING 68		

Db 61 plgtfndngvwtlqgqnlvavprdsyprctvavltckypealeqgrgdpilyiqn 120
 QY 69 KDLCECAEIOGKPTLOLKEKNIMDLVEKKAOKPFLPEFHNKEGSTSVFOSVSGMFLA 128
 Db 121 pemclcyckevgepbtqlkqgkmdlygqpevpkpfilytraktstclsevalpdmfla 180
 QY 129 TSTSGOPIFLTKERGITNNNTNFYLD 154
 Db 181 sakrd-qpliltseigksyntafeln 205

RESULF 15

AAW86286
 ID AAW86286 standard; Protein; 160 AA.

AAW86286;

19-FEB-1999 (first entry)

Rodent interleukin (IL)-1 epsilon polypeptide.

Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine; inflammatory response; immune system; diagnosis; agonist; antagonist; chemokine.

Mus sp.

W09847921-A1.

29-OCT-1998.

17-APR-1998; 98WO-US06879.

06-AUG-1997; 97US-005511.

21-APR-1997; 97US-0837627.

(SCHE) SCHERING CORP.

Bazan JF, Hedrick JA, Kastelein RA, Sana TR;

WPI; 1998-609976/51.

N-PSDB; AAV71960.

Claim 1; Pages 92-93; 113pp; English.

This represents a rodent interleukin (IL)-1 epsilon polypeptide. The invention relates to a recombinant polypeptide that specifically binds polyclonal antibodies (Abs) generated against a 12 consecutive amino acid segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these IL polypeptides are used to regulate a cell involved in an inflammatory response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are used to produce Abs and antigen-Abs complexes. The polypeptides, Abs and the corresponding nucleic acids regulate development and/or the immune system, and can be used to diagnose and treat conditions associated with abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1 epsilon polypeptides are used with agonists or antagonists of IL-1 alpha, IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1 epsilon polypeptides may be used as a soluble polypeptide or as a fusion protein with another cytokine or chemokine.

Sequence 160 AA;

Query Match 35.9%; Score 293.5; DB 19; Length 160;

Best Local Similarity 37.7%; Pred. No. 1e-24;

Matches 58; Conservative 31; Mismatches 62; Indels 3; Gaps 1;

1 MNPORE--AAPKSYAIDSRQMWVWVLSGNSLIAPLRSIKPVTLILACRDTFSDKE 57

Db 1 mkekelraaspslrhvgdlsrswllqnnlltavprkqetvptitllpcqylatletn 60
 QY 58 KGNWVYLGIRKRDCLFCAEIOGKPTLOLKEKNIMDLVEKKAOKPFLPEFHNKEGSTSVF 117
 Db 61 rgdptymgvqrpmsci fctkdgeqpvqlgqgnimemynkkkevksalfyhkksqststf 120
 QY 118 QSVSYPGWFIASTSTSGOPIFLTKERGITNNNTNF 151
 Db 121 esaafpgwfiavcskyscp11ltgelgelftidf 154

Search completed: May 10, 2002, 09:11:45
 Job time: 115 sec

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OM protein - protein search, using sw model

Run on: May 10, 2002, 09:10:20 ; Search time 14.4 Seconds
(without alignments)
830.514 Million cell updates/sec

Title: US-09-723-676-2

Perfect score: 818
Sequence: 1 MNFOREAPKSYAIRDSROM.....FLTKERGITNNFYLSVE 157

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	200.5	24.5	155	2	JC7104	interleukin-1 rece
2	195.5	23.9	178	2	A44610	interleukin-1 rece
3	183.5	22.4	178	2	C40956	interleukin-1 rece
4	182	22.2	177	2	A30386	interleukin-1 rece
5	178.5	21.8	180	2	A39386	interleukin-1 rece
6	170.5	20.8	177	2	A54377	interleukin-1 beta
7	165.5	20.0	266	1	ICB01B	interleukin-1 beta
8	163.5	20.0	266	1	S23010	interleukin-1 beta
9	163.5	20.0	269	1	ICB01B	interleukin-1 beta
10	158.5	19.4	267	1	JN0724	interleukin-1 beta
11	158.5	19.4	267	1	S38373	interleukin-1 beta
12	158.5	19.4	268	1	A30584	interleukin-1 beta
13	158	19.3	269	1	IS5969	interleukin-1 beta
14	155.5	19.0	214	2	JC5646	interleukin-1 beta
15	88.5	10.8	268	1	A61246	interleukin-1 alph
16	84.5	10.3	268	1	ICB01A	interleukin-1 alph
17	78	9.5	534	2	S56785	TCPI-related prote
18	77.5	9.5	786	2	E86268	hypothetical prote
19	77	9.4	493	2	T19383	hypothetical prote
20	76.5	9.4	270	2	I46620	interleukin-1 alph
21	76.5	9.4	1533	2	F71274	hypothetical prote
22	75.5	9.2	270	1	S10532	interleukin-1 alph
23	75	9.2	520	2	S45753	probable membrane
24	74.5	9.1	386	2	S49218	histidine decarbox
25	74	9.0	269	2	S16671	Dd31 protein - S11
26	74	9.0	932	2	G86857	isolectine-CRNA 1
27	74	9.0	1101	2	T26919	hypothetical prote
28	73.5	9.0	309	2	B86162	hypothetical prote
29	73.5	9.0	376	2	T39056	hypothetical prote

30	73	8.9	585	2	T50325	probable ubiquitin
31	73	8.9	1045	2	B30239	hydroxymethylgluta
32	72.5	8.9	197	2	T46496	hypothetical prote
33	72.5	8.9	394	2	D65167	probable membrane
34	72	8.8	268	1	B24073	interleukin-1 alph
35	72	8.8	417	1	S20608	heat shock protein
36	72	8.8	418	2	I52968	colligin-2 - human
37	71.5	8.7	555	2	B72341	uridine kinase-rel
38	71.5	8.7	871	2	S68482	probable membrane
39	71.5	8.7	1058	1	GNEF17	retrovirus-related
40	71	8.7	270	1	ICMS1	interleukin-1 alph
41	71	8.7	454	2	A41659	benzoate 1,2-dioxy
42	71	8.7	87	2	A41659	100 kDa coactivato
43	70.5	8.6	342	2	S76680	hypothetical prote
44	70.5	8.6	522	2	S75491	hypothetical prote
45	70.5	8.6	712	2	E81196	transferrin-bindin

ALIGNMENTS

RESULT 1
JC7104
interleukin-1 receptor antagonist - human
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ext_change 21-Jul-2000
C:Accession: JC7104
R:Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A>Title: IL1RH1: A novel interleukin-1 receptor antagonist gene.
A:Reference number: JC7104; MUID:9443727
A:Accession: JC7104
A:Molecule type: mRNA
A:Residues: 1-155 <MUI>
A:Cross-references: GB:AF186094; NID:g6049804; PIDN:AAF02757.1; PID:g6049805
C:Genetics:
A:Gene: IL1RH1
A:Map position: 2q14
C:Keywords: macrophage

Query Match 24.5%; Score 200.5; DB 2; Length 155;
Best Local Similarity 35.1%; Pred. No. 1.1e-12;
Matches 54; Conservative 24; Mismatches 61; Indels 15; Gaps 6;
QY 12 VAIRDSROWWVLSGNSLIAPL--SRSIKPYLHLIACR--DTEFSDKEGNNVYLGIR 67
DB 9 FRKKDALKVLYLHNNQLLAGLHAGKVIKGEISVVPNRMIDASTSP-----VILGVQ 62
QY 68 GKDLCFCAEIOGKPTIOLKEKNIMLYEKKAKOPLFEHNKSGSYQSVSPGWEI 127
DB 63 GGSQCLSCG-VGQEPPLTLEPVNIMELYLGAKESKSTFYRRDMGLTSSFSAAYPGWFL 121
QY 128 ATSTSGOPFLTK--ERGITTNN--TNFYLSVE 157
DB 122 CTVPEADQPVRLQLPENGGMNAPITDFYFOQCD 155
RESULT 2
A44610
interleukin-1 receptor antagonist precursor - mouse
M:Alternate names: IL-1Ra
C:Species: Mus musculus (house mouse)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #ext_change 16-Jul-1999
C:Accession: A44610; B40956; A49031; I56106; I52970
R:Matsumura, H.; Roussel, M.F.; Matsumura, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A>Title: Cloning and expression of murine interleukin-1 receptor antagonist in macroph
A:Reference number: A44610; MUID:91316273
A:Accession: A44610
A:Molecule type: mRNA
A:Residues: 1-178 <MAT>
A:Cross-references: GB:M64404; NID:g198296; PIDN:AAA39277.1; PID:g198297

R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
 A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
 A:Accession: A40956; MUID:91271363
 A:Accession: B40956
 A:Molecule type: DNA
 A:Residues: 7-178 <EIS>
 A:Cross-references: GB:M63100; NID:g198389; PIDN:AAA9310.1; PID:g198390
 R:Shuck, M.E.; Bessaly, T.E.; Tracey, D.E.; Bienkowski, M.J.
 Eur. J. Immunol. 21, 2775-2780, 1991
 A:Title: Cloning, heterologous expression and characterization of murine interleukin 1
 A:Reference number: A45031; MUID:92037824
 A:Accession: A45031
 A:Molecule type: mRNA
 A:Residues: 23-178 <SHU>
 A:Cross-references: GB:S64082; NID:g238584; PIDN:AAB20265.1; PID:g238585
 A:Experimental source: peritoneal macrophages, ICR strain
 R:Zahedi, K.; Seidlin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
 J. Immunol. 146, 4228-4233, 1991
 A:Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map
 A:Reference number: I56106; MUID:91250712
 A:Accession: I56106
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-178 <RES>
 A:Cross-references: GB:M74294; NID:g198387; PIDN:AAA9310.1; PID:g198388
 R:Zahedi, K.A.; Uhlir, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
 Cytokine 6, 1-9, 1994
 A:Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat
 A:Reference number: I52970; MUID:94271931
 A:Accession: I52970
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-178 <RE2>
 A:Cross-references: GB:J32838; NID:g487864; PIDN:AAA20576.1; PID:g528978
 A:Gene: IL-1rn
 C:Genetics:
 A:Introns: 40/2; 70/1; 107/3
 C:Superfamily: Interleukin-1
 C:Keywords: cytokine receptor
 F:1.26/Domain: signal sequence #status predicted <SIG>
 F:27-178/Product: Interleukin-1 receptor antagonist #status predicted <MA2>
 Query Match 23.9%; Score 195.5; DB 2; Length 178;
 Best Local Similarity 33.6%; Pred. No. 4.1e-12;
 Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;
 Oy 4 OREAPKSYAIRDSROMVWVLSGNSLIAPL-SRSIK-----PVLHLIACRDTFEFS 54
 Db 31 KRPKMOMAFRIWDNOKTFYLRNNQILAGYLOGPNKLEKIDVPIDEFN----- 80
 Oy 55 DKEKNMYYLIGIKGKDLCECAEIOGKPTQLKEKNIMDYVERKAOPFLFFHNKEGST 114
 Db 81 -----SVFLGIHGKLTCLSCAKSGSDIKQLDEVNITDLSKKNEDKRRFTFISSEKPT 134
 Oy 115 SVFOSVSTPGWFIATSTTSGQPIFLT 140
 Db 135 TSFESACPGWFLCTTLEADRPVSLT 160
 RESULT 3
 C40956
 Interleukin-1 receptor antagonist precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
 C:Accession: C40956
 R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
 A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
 A:Reference number: A40956; MUID:91271363
 A:Accession: C40956

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-178 <EIS>
 A:Cross-references: GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g204929
 C:Superfamily: Interleukin-1
 C:Keywords: cytokine receptor
 Query Match 22.4%; Score 183.5; DB 2; Length 178;
 Best Local Similarity 31.9%; Pred. No. 6.4e-11;
 Matches 45; Conservative 26; Mismatches 55; Indels 15; Gaps 2;
 Oy 4 OREAPKSYAIRDSROMVWVLSGNSLIAPL-SRSIKPTVHLIACRDTFEFSKEXG 59
 Db 31 KRPKMOMAFRIWDNOKTFYLRNNQILAGYLOGPNKLEKIDVPIDEFN----- 81
 Oy 60 MNVYLIGIKGKDLCECAEIOGKPTQLKEKNIMDYVERKAOPFLFFHNKEGSTSVFOS 119
 Db 82 -VFLGIHGKLTCLSCVSGSDTKQLDEVNITDLSKKNEDKRRFTFISSEKPTFSFS 139
 Oy 120 VSYPGWFIATSTTSGQPIFLT 140
 Db 140 LACPGWFLCTTLEADRPVSLT 160
 RESULT 4
 A30368
 Interleukin-1 receptor antagonist secreted form precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000
 C:Accession: A40956; I37894; A30368; S08159; S08159; A37822
 R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
 A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami
 A:Reference number: A40956; MUID:91271363
 A:Accession: A40956
 A:Molecule type: DNA
 A:Residues: 1-177 <EIS>
 A:Cross-references: GB:M63099; NID:g186385; PIDN:AAB41943.1; PID:g186386
 R:Gennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari
 Cytokine 4, 83-89, 1992
 A:Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonis
 A:Reference number: I37894; MUID:92338323
 A:Accession: I37894
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-177 <LEN>
 A:Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799
 R:Cartier, D.B.; Delbel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom
 J.G.; Siew, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Helinikson, R.L.;
 Nature 344, 633-638, 1990
 A:Title: Purification, cloning, expression and biological characterization of an inte
 A:Reference number: A30368; MUID:90220867
 A:Accession: A30368
 A:Molecule type: mRNA
 A:Residues: 1-177 <CAR>
 A:Cross-references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579
 A:Note: parts of this sequence, including the amino end of the mature protein, were c
 R:Eisenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H
 Nature 343, 341-346, 1990
 A:Title: Primary structure and functional expression from complementary DNA of a huma
 A:Reference number: S08159; MUID:90136921
 A:Accession: S08159
 A:Molecule type: protein
 A:Status: not compared with conceptual translation
 A:Accession: S08160
 A:Molecule type: mRNA
 A:Residues: 1-177 <EIS>
 A:Cross-references: GB:X52015; NID:g32576; PIDN:CAA36262.1; PID:g32577
 R:Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Driggs, D.J.; Heimdal, P.L.;
 Nature 343, 336-340, 1990
 A:Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibito
 A:Reference number: S08159; MUID:90136920
 A:Accession: S08159
 A:Molecule type: protein

A:Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>
 R.Bienkowski, M.J.; Fessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde, J. Biol. Chem. 265, 14505-14511, 1990
 A:Title: Purification and characterization of interleukin 1 receptor level antagonist p
 A:Reference number: A37822; MUID:90354444
 A:Accession: A37822
 A:Molecule type: protein
 A:Residues: 26-52;70-77;122-127;170-175 <BIE>
 A:Experimental source: culture medium, PMA-stimulated THP-1 cells
 C:Comment: For an alternative splice form, see PIR:A39386
 C:Genetics:
 A:Gene: GDB: IL1RN
 A:Cross-references: GDB:125897; OMIM:147679
 A:Map position: 2q14.2-q14.2
 A:Introns: 39/2; 69/1; 106/3
 C:Superfamily: Interleukin-1
 C:Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:16-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>
 F:109/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 22.2%; Score 182; DB 2; Length 177;
 Best Local Similarity 27.9%; Pred. No. 8; 9e-11;
 Matches 46; Conservative 27; Mismatches 64; Indels 28; Gaps 4;
 Oy 4 GREAPKSAVIRDSROMVWVLSGNSLIAPLSR-----SIKVTYLLIACRDTFES 54
 Db 30 RKSSKQAFRIWDVNOKTFILRNQIVAGYLOGPNVLEEKIDVPLEPHAL----- 81
 Oy 55 DKEGMMVYLGKGDLCFCAEIQGKPTLOLKEKNIMDLVEKKAOKPFLFFHNKEGST 114
 Db 82 -----FLGIHGKMKCLSCVKSGETRLQLEAVNITDLSENRKODKRAFIKSDSGPT 133
 Oy 115 SVFOSVYPGWFIATSTSGQPIFLTK--ERGITNNTFYLDVSE 157
 Db 134 TSFESACPGWFLCTAMEADQPVSLTNPDEGVN-VTKFYFQDE 177

RESULT 5
 A39386
 Interleukin-1 receptor antagonist, long intracellular splice form - human
 N:Contains: Interleukin-1 receptor antagonist, short intracellular splice form
 C:Species: Homo sapiens (man)
 C:Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
 C:Accession: I37893; A39386
 R:Muñoz, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovan J. Exp. Med. 182, 623-628, 1995
 A:Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant
 A:Reference number: I37893; MUID:95355865
 A:Accession: I37893
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1180 <RES>
 A:Cross-references: EMBL:X84348; NID:91008970; PIDN:CAA59087.1; PID:91008971
 R:Ashkili, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Biglier, C.F.; Jaffe, G.J.; Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
 A:Title: CDNA cloning of an intracellular form of the human interleukin 1 receptor antag
 A:Reference number: A39386; MUID:91219436
 A:Accession: A39386
 A:Molecule type: mRNA
 A:Residues: 1-3;25-180 <HAS>
 A:Cross-references: GB:M55646; NID:9186291; PIDN:AAA59138.1; PID:9186292
 C:Comment: For an alternative splice form, see PIR:A30368
 C:Genetics:
 A:Gene: GDB: IL1RN
 A:Cross-references: GDB:125897; OMIM:147679
 A:Map position: 2q14.2-q14.2
 C:Superfamily: Interleukin-1
 C:Keywords: alternative splicing; cytokine receptor
 F:1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #stat
 F:1-3;25-180/Product: interleukin-1 receptor antagonist, short intracellular splice form

Query Match 22.2%; Score 182; DB 2; Length 180;
 Best Local Similarity 27.9%; Pred. No. 9; 1e-11;
 Matches 46; Conservative 27; Mismatches 64; Indels 28; Gaps 4;

Oy 4 GREAPKSAVIRDSROMVWVLSGNSLIAPLSR-----SIKVTYLLIACRDTFES 54
 Db 33 RKSSKQAFRIWDVNOKTFILRNQIVAGYLOGPNVLEEKIDVPLEPHAL----- 84
 Oy 55 DKEGMMVYLGKGDLCFCAEIQGKPTLOLKEKNIMDLVEKKAOKPFLFFHNKEGST 114
 Db 85 -----FLGIHGKMKCLSCVKSGETRLQLEAVNITDLSENRKODKRAFIKSDSGPT 136
 Oy 115 SVFOSVYPGWFIATSTSGQPIFLTK--ERGITNNTFYLDVSE 157
 Db 137 TSFESACPGWFLCTAMEADQPVSLTNPDEGVN-VTKFYFQDE 180

RESULT 6
 A54377
 Interleukin-1 receptor antagonist secreted form precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
 C:Accession: A54377; I46729
 R:Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M J. Biol. Chem. 269, 6962-6971, 1994
 A:Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional ch
 A:Reference number: A54377; MUID:94165101
 A:Accession: A54377
 A:Molecule type: mRNA
 A:Residues: 1-177 <COM>
 A:Cross-references: GB:S68977; NID:9545740; PIDN:AAB30093.1; PID:9545741
 A:Experimental source: colon tissue
 A:Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBI:P:144169)
 R:Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Mori, S.; Furukawa, S.; Ma Immunology 77, 235-244, 1992
 A:Title: Interleukin-1 receptor antagonist in inflammatory exudate cells of rabbits. P
 A:Reference number: I46729; MUID:93052512
 A:Accession: I46729
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-177 <GOT>
 A:Cross-references: GB:D21832; NID:9425787; PIDN:BA04860.1; PID:94252205
 C:Superfamily: Interleukin-1
 C:Keywords: cytokine receptor; extracellular protein; glycoprotein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.8%; Score 178.5; DB 2; Length 177;
 Best Local Similarity 31.2%; Pred. No. 2e-10;
 Matches 45; Conservative 21; Mismatches 57; Indels 21; Gaps 2;
 Oy 4 GREAPKSAVIRDSROMVWVLSGNSLIAPLSR-----APLSRSIKPVYLLIACRDTFESDK 56
 Db 30 KRCKRQAFRIWDVNOKTFILRNQIVAGYLOGPNVLEEKIDVPLEPHAL----- 76
 Oy 57 EKGMMVYLGKGDLCFCAEIQGKPTLOLKEKNIMDLVEKKAOKPFLFFHNKEGSTV 116
 Db 77 -EPQLFLGIQGRKCLSCVKSGETRLQLEAVNITDLSENRKODKRAFIKSDSGPTT 135
 Oy 117 FOSVYPGWFIATSTSGQPIFLTK 140
 Db 136 TSFESACPGWFLCTAMEADQPVSLTNPDEGVN-VTKFYFQDE 159

RESULT 7
 ICB01B
 Interleukin-1 beta precursor - bovine
 N:Alternate names: hematopoietin-1; IL-1 beta
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
 C:Accession: J10010; S01380

R:Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.; Mol. Immunol. 25, 429-437, 1988
 A:Title: Cloning, sequence and expression of bovine Interleukin 1-alpha and interleukin 1-beta.
 A:Reference number: A94695; MUID:88318652
 A:Accession: J00010
 A:Molecule type: mRNA
 A:Residues: 1-266 <MAL>
 A:Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
 A:Leong, S.R.; Flagg, G.M.; Lawman, M.; Gray, P.W.
 Nucleic Acids Res. 16, 9054, 1988
 A:Title: The nucleotide sequence for the cDNA of bovine Interleukin-1 beta.
 A:Reference number: S01380; MUID:89016591
 A:Accession: S01380
 A:Molecule type: mRNA
 A:Residues: 1-251, 'A', 253-266 <LEO>
 A:Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449
 C:Comment: This protein is a cytokine that mediates a variety of immunoregulatory and in vivo form of Interleukin-1beta, unlike Interleukin 1-alpha, is inactive.
 C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage of Interleukin-1beta precursor is less heavily myristoylated than Interleukin-1a
 C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F:114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match 20.8%; Score 170.5; DB 1; Length 266;
 Best Local Similarity 31.4%; Pred. No. 2e-09;
 Matches 48; Conservative 33; Mismatches 51; Indels 21; Gaps 5;

OY 14 IRDSRQWVWISGNSLIAPLSRSIKPVTHLHIA---CRDTEF-----SDKEKGM--VY 63
 DB 123 LQDRQKSLVTLASPCVILKA-----LHLSQEMNREVFCMSFVGGERDKKIPVA 172
 OY 64 LGIKGKDLCLFCAEIQGKPTLQKEKNIMDLVEYKAKQPFLEFHNKGSVSFQSVSP 123
 DB 173 LGIKKKNLTLSCVKKGDPTLQLEVD-PRVYPRKRNKEKFEVTEIKNTVERESVLYP 231
 OY 124 GWFATSTTSGQPIFLTKRGITNTNFYLDVS 156
 DB 232 NWYISTQIEPRPVFLGHRGQDIDTFRMETL 264

RESULT 8
 S23010
 Interleukin-1 beta precursor - sheep
 N:Alternate names: hematopoietin-1; IL-1 beta
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C>Date: 08-Jun-1994 #sequence-revision 22-Nov-1996 #text-change 15-Oct-1999
 C:Accession: S23010; S43047; S13092; B61246
 R:Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
 DNA Seq. 1, 423-426, 1991
 A:Title: Nucleotide sequence of ovine macrophage Interleukin-1 beta cDNA.
 A:Reference number: S23010; MUID:92119335
 A:Accession: S23010
 A:Molecule type: mRNA
 A:Residues: 1-266 <SEO>
 A:Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809
 A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an addi
 R:Sargan, D.R.
 submitted to the EMBL Data Library, May 1992
 A:Reference number: S43047
 A:Accession: S43047
 A:Molecule type: mRNA
 A:Residues: 1-13, 'C', 15-54, 'K', 56-63, 'A', 65-144, 'U', 146-266 <SAR>
 A:Cross-references: EMBL:X54796; NID:g1273; PIDN:CAA8556.1; PID:g1274
 R:Flislerstrand, C.; Sargan, D.
 Nucleic Acids Res. 18, 7165, 1990
 A:Title: Nucleotide sequence of ovine Interleukin-1 beta.
 A:Reference number: S13092; MUID:91088326
 A:Accession: S13092
 A:Molecule type: mRNA
 A:Residues: 1-13, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'U', 146-266 <FIS>
 A:Cross-references: EMBL:X54796

A:Note: the authors translated the codon AGT for residue 62 as Arg
 R:Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
 Immunology 74, 453-460, 1991
 A:Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
 A:Reference number: A61246; MUID:92120716
 A:Accession: B61246
 A:Molecule type: mRNA
 A:Residues: 1-144, 'U', 146-266 <AND>
 C:Comment: This protein lacks a conventional signal sequence for protein export. Clea
 ved form of Interleukin-1beta, unlike Interleukin 1-alpha, is inactive.
 C:Comment: Interleukin-1beta precursor is less heavily myristoylated than Interleukin
 C:Genetics:
 A:Gene: IL-1-beta
 C:Superfamily: Interleukin-1
 C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F:114-266/Product: Interleukin-1 beta #status predicted <MAT>

Query Match 20.4%; Score 166.5; DB 1; Length 266;
 Best Local Similarity 29.2%; Pred. No. 5.1e-09;
 Matches 42; Conservative 38; Mismatches 61; Indels 3; Gaps 3;

OY 14 IRDSRQWVWISGNSLIAPLSRSIKPVTHLHIAQRD-TEFSDKEKGMVYLGKGDLC 72
 DB 123 LQDRQKSLVTLASPCVILKA-LHLSQEMNREVFCMSFVGGERDKKIPVALGTRDKNLY 181
 OY 73 LQCAEIQGKPTLQKEKNIMDLVEYKAKQPFLEFHNKGSVSFQSVSPGWFITSTT 132
 DB 182 LSCVKKGDPTLQLEVD-PRVYPRKRNKEKFEVTEIKNTVERESVLYPMWYISTQT 240
 OY 133 SGQPIFLTKRGITNTNFYLDVS 156
 DB 241 EKKPVFLGHRGQDIDTFRMETL 264

RESULT 9
 ICHU1B
 Interleukin-1 beta precursor [validated] - human
 N:Alternate names: hematopoietin-1; IL-1 beta
 C:Species: Homo sapiens (man)
 C>Date: 28-Feb-1986 #sequence-revision 15-May-1998 #text-change 15-Sep-2000
 C:Accession: A25542; A29019; A9361; I51852; I65200; I38132; B27616; A01848;
 R:Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.
 Nucleic Acids Res. 14, 7897-7914, 1986
 A:Title: Genomic sequence for human proliferin Interleukin 1 beta: possible evolution from a
 A:Reference number: A25542; MUID:87040762
 A:Accession: A25542
 A:Molecule type: DNA; mRNA
 A:Residues: 1-5, 'K', 7-269 <CLA>
 A:Cross-references: GB:X04500; NID:g33788
 A:Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu
 R:Bensi, G.; Rangel, G.; Palla, E.; Carinchi, V.; Buonamassa, D.T.; Meli, M.
 Gene 52, 95-101, 1987
 A:Title: Human Interleukin-1 beta gene.
 A:Reference number: A29019; MUID:87248099
 A:Accession: A29019
 A:Molecule type: DNA
 A:Residues: 1-269 <BEN>
 A:Cross-references: GB:M15640; NID:g186281; PIDN:AAA74137.1; PID:g386816
 R:Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Din
 Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
 A:Title: Nucleotide sequence of human monocyte Interleukin 1 precursor cDNA.
 A:Reference number: A94023; MUID:85088517
 A:Accession: A94023
 A:Molecule type: mRNA
 A:Residues: 1-5, 'K', 7-269 <AUR>
 A:Cross-references: GB:K02770; NID:g186268; PIDN:AAA36106.1; PID:g307043
 R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Breed, G.; Price, V.; Gillis,
 Nature 315, 641-647, 1985
 A:Title: Cloning, sequence and expression of two distinct human Interleukin-1 complem
 A:Reference number: A9361; MUID:85240547
 A:Accession: A9361
 A:Molecule type: mRNA

[illegible]

10.8%; Score 88.5; DB 1; Length 268;

Search completed: May 10, 2002, 09:12:07
Job time: 107 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 10, 2002, 09:11:00 ; Search time 11.69 Seconds

(without alignments)
492.419 Million cell updates/sec

Title: US-09-723-676-2

Perfect score: 818
Sequence: 1 MNFORAPKSYAIRDSRQ.....FLTKRGITNTNFIQDSVE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	195.5	23.9	178 1 IL1X_MOUSE	P25085 mus musculus
2	183.5	22.4	178 1 IL1X_RAT	P25086 rattus norv
3	182	22.2	177 1 IL1X_HUMAN	P18510 homo sapien
4	181	22.1	177 1 IL1X_HUMAN	O18999 equus caball
5	178.5	21.8	177 1 IL1X_RABIT	P26890 oryctolagus
6	178	21.8	177 1 IL1X_PIG	O29056 sus scrofa
7	173	21.1	174 1 IL1X_BOVIN	O77482 bos taurus
8	166.5	20.4	266 1 IL1B_SHEEP	P21621 ovis aries
9	164.5	20.1	266 1 IL1B_BOVIN	P09428 bos taurus
10	163.5	20.0	269 1 IL1B_HUMAN	P01584 homo sapien
11	161.5	19.7	267 1 IL1B_FELCA	P16687 felis silve
12	159.5	19.5	266 1 IL1B_CEREL	P51745 cervus elap
13	158.5	19.4	267 1 IL1B_PIG	P26889 sus scrofa
14	158.5	19.4	268 1 IL1B_HORSE	Q28386 equus caball
15	158.5	19.4	268 1 IL1B_MACFA	P79182 macaca fasc
16	158.5	19.4	268 1 IL1B_RABIT	P14628 oryctolagus
17	158.5	19.4	269 1 IL1B_MACMU	P48090 macaca mula
18	158.5	19.4	269 1 IL1B_MACNE	P51493 macaca neme
19	158	19.3	269 1 IL1B_MOUSE	P10749 mus musculu
20	157.5	19.3	266 1 IL1B_CAPHI	P79162 capra hircu
21	151.5	18.5	269 1 IL1B_CERTO	P46648 cercocebus
22	147.5	18.0	268 1 IL1B_RAT	O63264 rattus norv
23	90.5	11.1	268 1 IL1A_CAPHI	P79161 capra hircu
24	87	10.6	270 1 IL1A_FELCA	O46613 felis silve
25	85	10.4	268 1 IL1A_SHEEP	O46613 felis silve
26	84.5	10.3	268 1 IL1A_BOVIN	P08831 bos taurus
27	80.5	9.8	270 1 IL1A_HORSE	Q28385 equus caball
28	78	9.5	534 1 TCPCG_YEAST	P39077 saccharomyc
29	77	9.4	281 1 EFID_MOUSE	P57776 mus musculu
30	75.5	9.2	265 1 IL1A_CANFA	O46612 canis famli
31	75.5	9.2	270 1 IL1A_PIG	P18430 sus scrofa
32	75	9.1	520 1 APN2_YEAST	P38207 saccharomyc
33	74.5	9.1	720 1 MK06_RAT	P27704 rattus norv

34	74	9.0	269 1 DD31_DICTDI	Q02465 dictyosteli
35	73	8.9	1045 1 HMD2_YEAST	P14684 saccharomyc
36	72.5	8.9	267 1 IL1A_RABIT	P04822 oryctolagus
37	72.5	8.9	394 1 SENC_ECOLI	P31436 escherichia
38	72	8.8	417 1 HS47_HUMAN	P29043 homo sapien
39	72	8.8	418 1 CBP2_HUMAN	P50454 homo sapien
40	71.5	8.7	426 1 YXCX_ASTLO	P58151 astasia ion
41	71.5	8.7	871 1 SC10_YEAST	Q06245 saccharomyc
42	71.5	8.7	1058 1 POL3_DROME	P04323 drosophila
43	71	8.7	270 1 IL1A_MOUSE	P01582 mus musculu
44	71	8.7	454 1 XYIX_PSEPU	P23099 pseudomonas
45	70.5	8.6	712 1 TBPB_NEIMB	Q9K0V0 neisseria m

ALIGNMENTS

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RESULT 1
ID IL1X_MOUSE STANDARD: PRT; 178 AA.
AC P25085;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL-1RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91250712; PubMed=1828262;
RA Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;
RT "Mouse IL-1 receptor antagonist protein. Molecular characterization,
RT gene mapping, and expression of mRNA in vitro and in vivo.";
RL J. Immunol. 146:4228-4233(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91316273; PubMed=1830498;
RA Matsushima H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;
RT "Cloning and expression of murine interleukin-1 receptor antagonist
RT in macrophages stimulated by colony-stimulating factor 1.";
RL Blood 78:616-623(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-SWISS;
RX MEDLINE=94271931; PubMed=8003626; Prada A.E., Whitehead A.S.;
RA Zahedi K.A., Uhler C.M., Rits M.,
RT "The mouse interleukin 1 receptor antagonist protein: gene structure
RT and regulation in vitro.";
RL Cytokine 6:1-9(1994).
RN [4]
RP SEQUENCE OF 7-178 FROM N.A.
RX MEDLINE=91271363; PubMed=1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandtner B.J., Thompson R.C.;
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN [5]
RP SEQUENCE OF 23-178 FROM N.A.
RX MEDLINE=92037824; PubMed=1834470;
RA Shuk M.E., Eessalu T.E., Tracey D.E., Bienkowski M.J.;
RT "Cloning, heterologous expression and characterization of murine
RT interleukin 1 receptor antagonist protein.";
RL Eur. J. Immunol. 21:2773-2780(1991).
CC -I- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA BELONGS TO THE IL-1 FAMILY.
CC -I- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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RT "Primary structure and functional expression from complementary DNA
 of a human interleukin-1 receptor antagonist.";
 RL Nature 343:341-346(1990).
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91271363; PubMed=1828896;
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
 Brandhuber B.J., Thompson R.C.;
 RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
 gene family: evolution of a cytokine control mechanism.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92338323; PubMed=1385987;
 RA Lennard A., Gorman P., Carrier M., Griffiths S., Soctney H.,
 Sheer D., Solari R.;
 RT "Cloning and chromosome mapping of the human interleukin-1 receptor
 antagonist gene.";
 RL Cytokine 4:83-89(1992).
 RN [15]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97146044; PubMed=8992991;
 RA Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
 Arend W.P., Smith M.F., Jr.;
 RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
 and inducible regulatory regions.";
 RL J. Immunol. 158:748-755(1997).
 RN [16]
 RP SEQUENCE OF 26-45.
 RX MEDLINE=90136920; PubMed=2137200;
 RA Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Drilpps D.J., C.,
 Heimdal P.L., Arnes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
 RT "Interleukin-1 receptor antagonist activity of a human interleukin-1
 inhibitor.";
 RL Nature 343:336-340(1990).
 RN [17]
 RP SEQUENCE OF 26-52.
 RX MEDLINE=90354444; PubMed=2143761;
 RA Bienkowski M.J., Eessalu T.E., Berger A.E., Trussdell S.E.,
 Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
 Heinrichson R.L., Chosay J.G., Tracey D.E.;
 RT "Purification and characterization of interleukin 1 receptor level
 antagonist proteins from THP-1 cells.";
 RL J. Biol. Chem. 265:14505-14511(1990).
 RN [18]
 RP SEQUENCE FROM N.A. (INTRACELLULAR FORM).
 RX MEDLINE=91219436; PubMed=1827201;
 RA Haskill S., Martin G., Van Le U., Morris J., Pearce A., Bigler C.F.,
 Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
 RT "cDNA cloning of an intracellular form of the human interleukin 1
 receptor antagonist associated with epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
 RN [19]
 RP STRUCTURE BY NMR.
 RX MEDLINE=92297633; PubMed=1534997;
 RA Stockman B.J., Schall T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
 Brunner D.P., Yem A.W., Delbel M.R., Jr.;
 RT "Secondary structure and topology of interleukin-1 receptor
 antagonist protein determined by heteronuclear three-dimensional NMR
 spectroscopy.";
 RL Biochemistry 31:5237-5244(1992).
 RN [110]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94320651; PubMed=8045306;
 RA Stockman B.J., Schall T.A., Strakalaitis N.A., Brunner D.P.,
 Yem A.W., Delbel M.R., Jr.;
 RT "Solution structure of human interleukin-1 receptor antagonist
 protein.";
 RL FEBS Lett. 349:79-83(1994).
 RN [111]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94320368; PubMed=8175703;
 RA Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,

RA Brandhuber B.J.;
 RT "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
 resolution.";
 RL J. Biol. Chem. 269:12874-12879(1994).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=95172072; PubMed=7867645;
 RA Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
 Akesson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
 RT "Refined crystal structure of the interleukin-1 receptor antagonist.
 Presence of a disulfide link and a cis-proline.";
 RL Eur. J. Biochem. 227:838-847(1995).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
 RX MEDLINE=97215904; PubMed=9062194;
 RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
 Sarubbi E., Akesson A., Bowlin T., Yanofsky S., Barrett R.W.;
 RT "A new cytokine-receptor binding mode revealed by the crystal
 structure of the IL-1 receptor with an antagonist.";
 RL Nature 386:194-200(1997).
 CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
 RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: SECRETED OR INTRACELLULAR (THE VARIANT
 FORM).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
 SPLICING.
 CC -1- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
 PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -1- DATABASE: NAME=Rad Systems' cytokine source book;
 WWW="http://www.rndsystems.com/cyl_cat/illra.html".
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M55646; AAA59138.1; -
 DR EMBL: M63099; AAB41943.1; -
 DR EMBL: X52015; CA936262.1; -
 DR EMBL: X53296; CA937386.1; -
 DR EMBL: X64532; CAA45832.1; -
 DR EMBL: U65590; AAB92268.1; -
 DR EMBL: U65590; AAB92270.1; -
 DR PIR: A30368; A30368.
 DR PIR: A37822; A37822.
 DR PIR: S08160; S08160.
 DR PIR: S08159; S08159.
 DR PIR: A40956; A40956.
 DR PIR: A39386; A39386.
 DR PDB: 1ITN; 30-APR-94.
 DR PDB: 2IRT; 15-OCT-94.
 DR PDB: 1IRP; 27-FEB-95.
 DR PDB: 1ILR; 07-FEB-95.
 DR PDB: 1ILT; 01-APR-95.
 DR PDB: 1IRA; 17-JUN-98.
 DR Aarhus/Ghent-2DPAGE; 7104; IEF.
 DR Aarhus/Ghent-2DPAGE; 7105; IEF.
 DR MIM: 147679; -
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR PRINTS: PR00264; INTERLEUKIN1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 KW Glycoprotein; Signal; Alternative splicing; 3D-structure.
 FT SIGNAL 1 25
 FT CHAIN 1 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
 FT PROTEIN.
 FT DISULFID 91 141
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT


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DR EMBL: M57526; AAA31374.1; -
DR EMBL: D21832; BAA04860.1; -
DR PIR: A54377; A54377.
DR HSSP: P18510; 111R.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR PRINTS: PRO0264; INTERLEUKIN1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 177
FT DISULFID 91 141
FT CARBOHYD 109 109
FT SEQUENCE 177 AA; 20214 MW; F5BC087F097FEFAF CRC64;

Query Match 21.8%; Score 178.5; DB 1; Length 177;
Best Local Similarity 31.2%; Pred. No. 2.4e-10;
Matches 45; Conservative 21; Mismatches 57; Indels 21; Gaps 2;

OY 4 QREAPKSAIADSRQMWVLSGSLIA-----APLSIKPVTLLHLCRDTFESDK 56
DB 30 KRPCMQAARIWDVNOKTFYLRNNQLVAGYLOGPNKLEERIDVPL----- 76
OY 57 EKGNNVYLIGKIGKDLCLFCAEIQGKPTLOLKEKINIMLYEKKAKQKPFLEFHNKSGSTV 116
DB 77 -EPOLLFLGICIGKCLCLSCVKSQDKMKLHLEAVNITDLGKNKDKRFTFIRNSGPTTT 135
OY 117 FQSVSYGWFIASTSTSGPIFLT 140
DB 136 FESASCPGWFICTALEADQPVSLT 159

RESULT 6
IL1X_PIG STANDARD: PRT; 177 AA.
AC Q29056;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN) (IRAP).
GN IL1RN OR IRAP1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CROSSBREED; TISSUE=Lung;
RA Yin J., Murtough M.P.;
RT "Characterization of IRAP in morphine treated pig.";
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
CC EMBL: L3849; AAA9424.1; -
CC InterPro: IPR000975; Interleukin_1.
CC Pfam: PF00340; IL1; 1.
CC PRINTS: PRO0264; INTERLEUKIN1.
CC SMART: SM00125; IL1; 1.
CC PROSITE: PS00253; INTERLEUKIN_1; 1.

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KW Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 177
FT DISULFID 91 141
FT CARBOHYD 109 109
FT SEQUENCE 177 AA; 20093 MW; 2114DC6119A95F9 CRC64;

Query Match 21.8%; Score 178; DB 1; Length 177;
Best Local Similarity 29.6%; Pred. No. 2.7e-10;
Matches 47; Conservative 20; Mismatches 66; Indels 26; Gaps 3;

OY 4 QREAPKSAIADSRQMWVLSGSLIA-----APLSIKPVTLLHLCRDTFESDK 54
DB 30 KRPCMQAARIWDVNOKTFYLRNNQLVAGYLOGPNKLEERIDVPL----- 79
OY 55 DKEGNNVYLIGKIGKDLCLFCAEIQGKPTLOLKEKINIMLYEKKAKQKPFLEFHNKSGST 114
DB 80 -----FVFLGIHGKCLCLSCVKSQDKMKLHLEAVNITDLGKNKDKRFTFIRNSGPTT 133
OY 115 SVFQSVSYGWFIASTSTSGPIFLT-ERGILNNNTFY 152
DB 134 TSFESACPGWFICTALEADQPVGLTTPKAAVKYTKFY 172

RESULT 7
IL1X_BOVIN STANDARD: PRT; 174 AA.
AC 077482;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN) (IRAP).
GN IL1RN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=98305607; PubMed=9643454;
RA Kiritawa R., Fukuda T., Yamanaka H., Hagiwara K., Goto M., Ooba Y., Yoshino T., Iwai H.;
RT "Enzymatic amplification and expression of bovine interleukin-1 receptor antagonist cDNA."
RL Vet. Immunol. Immunopathol. 62:197-208(1998).
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
CC EMBL: AB005148; BAA31854.1; -
CC InterPro: IPR000975; Interleukin_1.
CC Pfam: PF00340; IL1; 1.
CC PRINTS: PRO0264; INTERLEUKIN1.
CC SMART: SM00125; IL1; 1.
CC PROSITE: PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 174
FT DISULFID 89 139
FT CARBOHYD 107 107
FT SEQUENCE 174 AA; 2114DC6119A95F9 CRC64;

```


CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M35589; AAA30585.1; -;
DR EMBL: X12498; CAA31018.1; -;
DR EMBL: M37211; AAA30584.1; -;
DR PIR: J10010; ICBO1B.
DR HSSP: P01584; 1H1B.
DR InterPro: IPR002348; Interleukin_1.
DR InterPro: IPR003502; Interleukin_1_prop.
DR Pfam: PF00340; IL1; 1.
DR PRINTS: PR00262; IL1HGF.
DR PRINTS: PR00264; INTERLEUKIN1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
DR CycloLine: Macrophage; Mltogen; Inflammatory response; Pyrogen.
FW PROPEP 1 113 INTERLEUKIN-1 BETA.
FT CHAIN 114 266
FT COMPLET 252 252 A -> G (IN REF. 2).
SQ SEQUENCE 265 AA: 30774 MW: 9018575070586 CRC64;

Query Match 20.1%; Score 164.5; DB 1; Length 266;
Best Local Similarity 30.7%; Pred. No. 8.7e-09;
Matches 47; Conservative 33; Mismatches 52; Indels 21; Gaps 5;

OY 14 IRDSQMWVYVLSGNSLIAPLSRSIKPVTILHIA---CRDTEF-----SPEKGNM--VY 63
DB 123 LQDRQKSLVSLASPCVLA-----LHLTQEMNREVPVCMSPVQEEERDKIPVA 172
OY 64 LGIKKRDCLFCAELQGRKTLQLEKKNIMDYERKAKRFLFPHNKGSTSVQSYSP 123
DB 173 LGIKKKNLYLSCVKKGDPDTLDLEVD-PKVVPRKNNKREVEYKTEIKNTVEESVLYP 231
OY 124 GWFATSTSGOPFLTKERGITNNTNFYLDV 156
DB 232 NWYISTQIEERPVLGHRRAQODITDFMETL 264

RESULT 10
IL1B_HUMAN STANDARD: PRT: 269 AA.
AC P01584;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 20-AUG-2001 (rel. 40, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA) (CATABOLIN).
GN IL1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85088517; PubMed=6083565;
RA Auron F.E., Webb A.C., Rosenwasser L.J., Mucci S.F., Rich A.,
RA Wolff S.M., Dinarello C.A.;

RT "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:7907-7911(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85240547; PubMed=2989698;
RA March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V.,
RA Gillis S., Henney C.S., Kronheim S.R., Grabstein K., Conlon P.J.,
RA Hopp T.P., Cosman D.;
RT "Cloning, sequence and expression of two distinct human interleukin-1
RT complementary DNAs.";
RL Nature 315:641-647(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87040762; PubMed=3490654;
RA Clark B.D., Collins K.L., Gandy M.S., Webb A.C., Auron P.E.;
RT "Genomic sequence for human prointerleukin 1 beta: possible evolution
RT from a reverse transcribed prointerleukin 1 alpha gene.";
RL Nucleic Acids Res. 14:7897-7914(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248099; PubMed=2954882;
RA Bensli G., Raugel G., Palla E., Carinci V., Buonamassa D.T., Melli M.;
RT "Human interleukin-1 beta gene.";
RL Gene 52:95-101(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=90249285; PubMed=2635664;
RA Kotenko S.V., Bulenkov M.T., Velko V.P., Epishin S.M., Iomakin I.B.,
RA Emel'yanov A.V., Kozlov A.P., Konusova V.G., Kotov A.Y.,
RA Kurdatova T.V., Reshetnikov V.L., Simbirtsev A.S., Kellinskii S.A.,
RA Vieterskii Y.P.;
RT "Cloning of the cDNA coding for human prointerleukin-1 alpha and
RT prointerleukin-1 beta.";
RL Dokl. Akad. Nauk SSSR 309:1005-1008(1989).
RN [6]
RP SEQUENCE FROM N.A.
RA Webb A.C., Dinarello C.A., Rosenwasser L.J., Mucci S.F., Rich A.,
RA Wolff S.M., Auron P.E.;
RT "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL Adv. Gene Technol. 22:339-340(1985).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=87156769; PubMed=3493774;
RA Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,
RA Nakai S., Hirai Y.;
RT "cDNA Cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell
RT line.";
RL Biochem. Biophys. Res. Commun. 143:345-352(1987).
RN [8]
RP SEQUENCE OF 117-128.
RX MEDLINE=88184226; PubMed=3281727;
RA Zsebo K.M., Wypych J., Yuschenko V.N., Lu H., Hunt P., Dukes P.P.,
RA Langley K.E.;
RT "Effects of hematopoietin-1 and interleukin 1 activities on early
RT hematopoietic cells of the bone marrow.";
RL Blood 71:962-968(1988).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=88211543; PubMed=3259176;
RA Priestle J.P., Schar H.-P., Grutter M.G.;
RT "Crystal structure of the cytokine interleukin-1 beta.";
RL EMBO J. 7:339-343(1988).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=90099325; PubMed=2602367;
RA Priestle J.P., Schar H.-P., Grutter M.G.;
RT "Crystallographic refinement of interleukin 1 beta at 2.0-A
RT resolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9667-9671(1989).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=90064532; PubMed=2585509;
RA Finzel B.C., Clancy L.L., Holland D.R., Muchmore S.W.,


```

RL Submitted (XXX-1993) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -I- SUBUNIT: MONOMER.
CC -I- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -I- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -I- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: M92060; AAA30814.1; -.
CC HSSP: P01584; I1IB.
CC InterPro: IPR002348; IL1_HBGF.
CC InterPro: IPR000975; Interleukin_1.
CC InterPro: IPR003502; Interleukin_1-prop.
CC Pfam: PF00340; IL1; 1.
CC Pfam: PF02394; IL1_propep; 1.
CC PRINTS: PR00262; IL1HBGF.
CC PRINTS: PR00125; IL1; 1.
CC SMART: SM00125; IL1; 1.
CC PROSITE: PS00253; INTERLEUKIN_1; 1.
CC CYCLOKINE; Macrophage; Mitogen; Inflammatory response; Pyrogen.
CC PROPEP 1 115 BY SIMILARITY.
CC CHAIN 116 267 INTERLEUKIN-1 BETA.
CC SEQUENCE 267 AA; 30361 MW; 781F9971E32F6AE1 CRC64;
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Query Match 19.7%; Score 161.5; DB 1; Length 267;
Best Local Similarity 31.0%; Pred. No. 1.7e-08;
Matches 49; Conservative 25; Mismatches 59; Indels 25; Gaps 5;
OY 10 KSVATRDSONMVLGNSGLIAPLSRTKPYVLH-----IACRDFEFDKSGNM 61
DB 121 QDYTRDISQKSLVLSGSEIIRA-----LHLNGQNMNQVYRMSFVHSEENSK 170
OY 62 --VYIGIKGKDCIFCAETIQGKPTTOLKEKNIND--LYVEKKAQKPELFFHNKEGSTSVF 117
DB 171 IYVVICIKKNNLYLSCVMKDGKPTQLQLE--MDPKVYPRKKKREKRVFNKTEIKGVNEF 227
OY 118 QSVSYRGWFIATSTSGQPIFLTKERGITNTNTFYLDV 155
DB 228 ESSQEPNMYISTSQAEEMPVFLGNTKGGDITDFIMES 265
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RESULT 12
IL1B_CEREL
ID IL1B_CEREL STANDARD; PRT; 266 AA.
AC P51745;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Cervus elaphus (Red deer).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]

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RP SEQUENCE FROM N.A.
RA Lookhart E.A.;
RL Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -I- SUBUNIT: MONOMER.
CC -I- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -I- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -I- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: U20500; AAA62234.1; -.
CC HSSP: P01584; I1IB.
CC InterPro: IPR002348; IL1_HBGF.
CC InterPro: IPR000975; Interleukin_1.
CC InterPro: IPR003502; Interleukin_1-prop.
CC Pfam: PF00340; IL1; 1.
CC Pfam: PF02394; IL1_propep; 1.
CC PRINTS: PR00262; IL1HBGF.
CC PRINTS: PR00125; IL1; 1.
CC SMART: SM00125; IL1; 1.
CC PROSITE: PS00253; INTERLEUKIN_1; 1.
CC CYCLOKINE; Macrophage; Mitogen; Inflammatory response; Pyrogen.
CC PROPEP 1 113 BY SIMILARITY.
CC CHAIN 114 266 INTERLEUKIN-1 BETA.
CC SEQUENCE 266 AA; 30629 MW; 4F40BAE6FD9F060 CRC64;
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Query Match 19.5%; Score 159.5; DB 1; Length 266;
Best Local Similarity 30.1%; Pred. No. 2.6e-08;
Matches 46; Conservative 33; Mismatches 53; Indels 21; Gaps 5;
OY 14 IRDSRQMWVLSGNSLIAPLSRTKPYVLHLIA---CHDTER-----SDKEKGNM--YV 63
DB 123 LQDRQNSLIVLASPCVLKA-----LHLISQMSREVVFCMSFYQAEERDNKIPVA 172
OY 64 LGIKGKDCIFCAETIQGKPTTOLKEKNINDLYVEKKAQKPELFFHNKEGSTSVFQSVSY 123
DB 173 LGIRKKNQYLSVCKKGDPTTQLQLEVD--PKVYPRKKMKEKRVFNKTEIKGVNEF 231
OY 124 GWFIASTSTSGQPIFLTKERGITNTNTFYLDV 156
DB 232 NWYISTSHPEEKPVFLGHRGGDITDFRMEYL 264
-----
RESULT 13
IL1B_PIG
ID IL1B_PIG STANDARD; PRT; 267 AA.
AC P26889;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314975; PubMed=8325511;
RA Huether M.J., Lin G., Smith D.M., Murtough M.P., Molitor T.W.;
RT "Cloning, sequencing and regulation of an mRNA encoding porcine
interleukin-1 beta.";
RL Gene 129:285-289(1993).
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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CC -----
CC DR EMBL; M86725; AAA02584.1; -.
CC DR PIR; JN0724; JN0724.
CC DR HSSP; P01584; 1H1B.
CC DR InterPro; IPR002348; IL1_HBGF.
CC DR InterPro; IPR000975; Interleukin_1.
CC DR InterPro; IPR003502; Interleukin_1-prop.
CC DR Pfam; PF00340; IL1; 1.
CC DR PRINTS; PR00262; IL1HBGF.
CC DR PRINTS; PR00264; INTERLEUKIN1.
CC DR SMART; SM00125; IL1; 1.
CC DR PROSITE; PS00253; INTERLEUKIN_1; 1.
CC DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
CC FT PROPEP 1 114 BY SIMILARITY.
CC FT CHAIN 115 267 INTERLEUKIN-1 BETA.
CC FT SEQUENCE 267 AA; 30404 MW; 7F6B92B784D5086F CRC64;
SQ
Query Match 19.4%; Score 158.5; DB 1; Length 267;
Best Local Similarity 29.1%; Pred. No. 3.3e-08;
Matches 44; Conservative 28; Mismatches 58; Indels 21; Gaps 4;
QY 14 IRDSQWVWVLSGNSLIAPLSRSIKPVTPLHLA--CRDTEF-----SDKEGKNVY 63
Db 124 LQDKHKSLVTLGPHMLKA-----LHLTLGDIKREVFCVMSVQGDSSNNKIPVT 173
QY 64 LGIKKDLCLFCALIQGKPTLQLEKKNIMDYVEKKAQKFFLEFHNKEGTSVFQSYSP 123
Db 174 LGIKKKNLYLSCVMDNFTLQLEDID-PRKRYPRKDEKRFVFYKTKKNVVEESALYP 232
QY 124 GWFATSTSTSGPFIPLTKRGRTTNNNTFYLD 154
Db 233 NWYISTSQAEQKPFVFLGNSKGRDITDFIWE 263
RESULT 14
ID IL1B_HORSE STANDARD: PRT; 268 AA.
AC 028386; 077744; 018995;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).

```

```

GN IL1B.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96131982; PubMed=8576682;
RA Kato H., Ohashi T., Nakamura N., Nishimura Y., Watari T., Goitsuka R.,
RA Tsujimoto H., Hasegawa A.;
RT "Molecular cloning of equine interleukin-1 alpha and -beta cDNAs.";
RL Vet. Immunol. Immunopathol. 48:221-231(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285941; PubMed=9622738;
RA Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT "Cloning of equine interleukin-1 alpha and equine interleukin-1 beta
RT and determination of their full-length cDNA sequences.";
RL Am. J. Vet. Res. 59:704-711(1998).
RN [3]
RP SEQUENCE FROM N.A. (SHORT FORM).
RX MEDLINE=97080493; PubMed=8921838;
RA Kato H., Yoon H.Y., Ohashi T., Watari T., Goitsuka R., Tsujimoto H.,
RA Hasegawa A.;
RT "Identification of an alternatively spliced transcript of equine
RT interleukin-1 beta.";
RL Gene 177:11-16(1996).
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
CC DR EMBL; D42147; BAA07718.1; -.
CC DR EMBL; U92481; AAC39256.1; -.
CC DR EMBL; D42165; BAA22528.1; -.
CC DR InterPro; IPR002348; IL1_HBGF.
CC DR InterPro; IPR000975; Interleukin_1.
CC DR InterPro; IPR003502; Interleukin_1-prop.
CC DR Pfam; PF00340; IL1; 1.
CC DR Pfam; PF02394; IL1_propep; 1.
CC DR PRINTS; PR00262; IL1HBGF.
CC DR PRINTS; PR00264; INTERLEUKIN1.
CC DR SMART; SM00125; IL1; 1.
CC DR PROSITE; PS00253; INTERLEUKIN_1; 1.
CC DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
CC Alternative splicing.
CC FT PROPEP 1 115 BY SIMILARITY.
CC FT CHAIN 116 268 INTERLEUKIN-1 BETA.
CC FT VARSPPLIC 101 154 MISSING (IN SHORT ISOFORM).
CC FT CONFLICT 45 45 D -> N (IN REF. 2).
CC FT CONFLICT 55 55 H -> Q (IN REF. 2).
CC FT CONFLICT 64 65 AM -> VV (IN REF. 2).

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FT CONFLICT 71 71 V -> M (IN REF. 2).
 FT CONFLICT 110 111 EG -> DD (IN REF. 2).
 FT CONFLICT 118 118 M -> V (IN REF. 2).
 FT CONFLICT 245 245 S -> K (IN REF. 2).
 SO SEQUENCE 268 AA; 30268 MW; 336F27792A1542EA CRC64;

Query Match 19.4%; Score 158.5; DB 1; Length 268;
 Best Local Similarity 30.5%; Pred. No. 3.3e-08;
 Matches 46; Conservative 25; Mismatches 59; Indels 21; Gaps 4;

QY 14 IRDSQMWVWVLSGNSLIAPLSRSIKPVTLLH-----IACRDTFSDEKRGNN-VY 63
 DB 125 LRDYHKSLSVSGACELQA-----VHLNGENTNOQVFCMSFVQGEETDKIPVA 174
 OY 64 LGIKGKDLFCFAEIQGKPTLQKEKNIMDIYERKAKRPFLEFNKSESTSVFQSYSP 123
 DB 175 LGLKKNLYLSCGMKDGKPTLQLETVD-PNTPYKRMKREKRVFNKMEIKGVFEESAMP 233
 QY 124 GWFIATSTTSGQPIFLTKERGITNNNTFYLD 154
 DB 234 NWYISTSOAKSPVFLGNTRGRDITDFTIME 264

RESULT 15
 IL1B_MACFA STANDARD; PRT; 268 AA.

AC P79182;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 GN IL1B.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RA Totsuka K., Takakura H., Hashimoto O., Tatsumi M.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.

CC -1- SUBUNIT: MONOMER.
 CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.

CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.

CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

CC EMBL: D63353; BAA09677.1; -.
 CC HSSP: P01584; 1H1B.
 CC InterPro: IPR002348; IL1_HBGF.
 CC InterPro: IPR000975; Interleukin_1.
 CC InterPro: IPR003502; Interleukin_1_prop.
 CC Pfam: PF00340; IL1; 1.
 CC Pfam: PF02394; IL1_propep; 1.

DR PRINTS: PR00262; IL1HBGF.
 DR PRINTS: PR00264; INTERLEUKIN1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 FT PROPEP 1 116 BY SIMILARITY.
 FT CHAIN 117 268 INTERLEUKIN-1 BETA.
 SO SEQUENCE 268 AA; 30425 MW; CFB7266E3E2C05B4 CRC64;

Query Match 19.4%; Score 158.5; DB 1; Length 268;
 Best Local Similarity 32.5%; Pred. No. 3.3e-08;
 Matches 51; Conservative 23; Mismatches 54; Indels 29; Gaps 6;

QY 14 IRDSQMWVWVLSGNSLIAPLSRSIKPVTLLH-----IACRDTFSDEKRGNN-VY 62
 DB 126 LRDQQLKSLVMSGPYELKA-----LHLQG-ODLEQOYVFSMSFVQGEESNDKIPV 174
 QY 63 YLGKGDLCFLCAEIQGKPTLQKE---KNIMDIYERKAKRPFLEFNKSESTSVFOS 119
 DB 175 ALGLKAKNLYLSCVAKDKDKPTQLQLESVDPKN---YPRKKMKREKRVFNKIEINNKLEFES 230
 QY 120 VSYGFWIATSTTSGQPIFLTKERGITNNNTFYLDV 156
 DB 231 AQFPNWYISTSOAESMPVFLGTRGQDITDFTMOFV 267

Search completed: May 10, 2002, 09:12:56
 Job time: 116 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 09:10:45 ; Search time 24.55 Seconds

(without alignments)
935.428 Million cell updates/sec

Title: US-09-723-676-2

Perfect score: 818

Sequence: 1 MNQREAPKSYAIRDSROM.....FLTKERGITNTNPFYLDSE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	818	100.0	157	4 Q9UHA5	Q9UHA5 homo sapien
2	516	63.1	183	11 Q9D6Z6	Q9D6Z6 mus musculu
3	452	55.3	164	4 Q9NZH7	Q9NZH7 homo sapien
4	385	47.1	158	4 Q9UHA7	Q9UHA7 homo sapien
5	345.5	42.2	169	4 Q9NZH8	Q9NZH8 homo sapien
6	293.5	35.9	160	11 Q9JLA2	Q9JLA2 mus musculu
7	229	28.0	192	4 Q9UHA6	Q9UHA6 homo sapien
8	229	28.0	218	4 Q9NZH6	Q9NZH6 homo sapien
9	229	28.0	218	4 Q9HBF3	Q9HBF3 homo sapien
10	200.5	24.5	155	4 Q9UBH0	Q9UBH0 homo sapien
11	198.5	24.3	155	11 Q9QYU1	Q9QYU1 mus musculu
12	198.5	24.3	156	11 Q9JIG2	Q9JIG2 mus musculu
13	195.5	23.9	159	11 Q70207	Q70207 mus musculu
14	182.5	22.2	178	4 Q9HBF2	Q9HBF2 homo sapien
15	182	22.2	180	4 Q14628	Q14628 homo sapien
16	181	22.1	143	4 Q9UPC0	Q9UPC0 homo sapien
17	176.5	21.6	176	6 Q9BEH0	Q9BEH0 canis famill
18	176	21.5	144	4 Q9BYX1	Q9BYX1 homo sapien
19	172	21.0	177	6 Q9GMZ4	Q9GMZ4 tursiops tr

20	166.5	20.4	176	6 Q9GKK2	Q9GKK2 canis famill
21	163.5	20.0	153	4 Q43645	Q43645 homo sapien
22	158.5	19.4	267	6 Q29082	Q29082 sus scrofa
23	154.5	18.9	266	11 Q9WVG1	Q9WVG1 cavia porcea
24	153.5	18.8	266	6 Q9TRK1	Q9TRK1 tursiops tr
25	142	17.4	267	13 Q73909	Q73909 gallus gall
26	140.5	17.2	269	6 Q9XS77	Q9XS77 trichosurus
27	130.5	16.0	276	13 Q57398	Q57398 cyprinus ca
28	130.5	16.0	276	13 Q9PW18	Q9PW18 cyprinus ca
29	128.5	15.7	260	13 Q9YGD3	Q9YGD3 oncorhynch
30	127.5	15.6	254	13 Q9PT12	Q9PT12 oncorhynch
31	124	15.2	283	13 Q9PVZ5	Q9PVZ5 xenopus lae
32	111.5	13.6	72	6 Q77771	Q77771 equus caball
33	104.5	12.8	272	13 Q9DDF2	Q9DDF2 cyprinus ca
34	101	12.3	272	13 Q9DDF3	Q9DDF3 cyprinus ca
35	83	10.1	118	6 Q9TSJ0	Q9TSJ0 equus caball
36	83	10.1	265	6 Q9TRK2	Q9TRK2 tursiops tr
37	80.5	9.8	547	5 Q9VIL1	Q9VIL1 drosophila
38	78.5	9.6	439	10 Q9FJV1	Q9FJV1 arabidopsis
39	77.5	9.5	786	10 Q9FZ71	Q9FZ71 arabidopsis
40	77.5	9.5	3529	5 Q9GP30	Q9GP30 theileria p
41	77	9.4	257	11 Q9CYJ5	Q9CYJ5 mus musculu
42	77	9.4	281	11 Q9CWM2	Q9CWM2 mus musculu
43	76.5	9.4	493	5 Q09479	Q09479 caenorhabd
44	76.5	9.4	1533	2 Q83826	Q83826 treponema p
45	76	9.3	880	11 P97693	P97693 rattus norv

ALIGNMENTS

RESULT 1
ID Q9UHA5 PRELIMINARY: PRT; 157 AA.
AC Q9UHA5:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Fill EYA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,
RT Sims J.E.,
RT "Four New Members Expand the IL-1 Superfamily.";
RT J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201833; AAF25213.1; -.
DR HSSP; P10749; 2MIB.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ SEQUENCE 157 AA; 17702 MW; 7A54F3D757A3EE3 CRC64;

Query Match 100.0%; Score 818; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.3e-76;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQREAPKSYAIRDSROMWVLSGNSLIAPLSRISIKPYTLHLIACRDTFSDKEKN 60
DB 1 MNQREAPKSYAIRDSROMWVLSGNSLIAPLSRISIKPYTLHLIACRDTFSDKEKN 60
QY MYVLGIKGDLCFCALIQCKPTLQLEKKNIMDLVYKKAQKPLFFHNKSGTSVQSV 120
DB MYVLGIKGDLCFCALIQCKPTLQLEKKNIMDLVYKKAQKPLFFHNKSGTSVQSV 120
QY 121 SYPGWFIATSTSGOPFLTKERGITNTNPFYLDSE 157
DB 121 SYPGWFIATSTSGOPFLTKERGITNTNPFYLDSE 157

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Db 121 SYGWFATSTSGOPILFKRGITNNNTNFEYLDSE 157
RESULT 2
AC 090626 PRELIMINARY; PRT; 183 AA.
ID 090626
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 231004N20RIK PROTEIN.
GN 231004N20RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Akawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Sakota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustlinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seyer T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tovo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontuski S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009787; BAB26505.1;
DR MGI: MGI:1916927. 231004N20RIK.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR PRODOM: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; UNKNOWN_1.
SO SEQUENCE 183 AA; 20878 MW; A3ACE339F96F02F CRC64;

Query Match 63.1%; Score 516; DB 11; Length 183;
Best Local Similarity 64.2%; Pred. No. 3.6e-45;
Matches 95; Conservative 24; Mismatches 29; Indels 0; Gaps 0;

QY 8 APKSAIDSRQWVWVLSGNSLIAPLSRSIKPVTLHLIACDTEFSDEKGNVYLGIG 67
Db 34 SPRNRYHDSQOMVAVLGNLTAVPASNVRKVVLSLACRTEFQDYKGNLVFLGIG 93
QY 68 GKDLCECAEIQGKPTQLQKEKNIMDLYEKKAKQPFLEFHNKEGTSVSQSVYSGWFI 127
Db 94 NRNLCEFCVEHEGKPTQLQKEVDIMNLYEKRAQKAPFLFHIGEGTSVSQSVYSGWFI 153
QY 128 ATSTTSGOPILFKRGITNNNTNFEYLDSE 155
Db 154 ATSSIERQITILFHQRGLVNTNFEYIES 181

RESULT 3
ID 09N2H7 PRELIMINARY; PRT; 164 AA.
AC 09N2H7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE INTERLEUKIN-1 HOMOLOG 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OSTEOCLASTOMA;
RX MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
DR EMBL: AF200494; AAF69250.1;
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
SO SEQUENCE 164 AA; 18521 MW; FDD2099FAA357A0A CRC64;

Query Match 55.3%; Score 452; DB 4; Length 164;
Best Local Similarity 94.6%; Pred. No. 1.1e-38;
Matches 88; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MNQREAPPSYAIRDSRQWVWVLSGNSLIAPLSRSIKPVTLHLIACDTEFSDEKGN 60
Db 1 MNQREAPPSYAIRDSRQWVWVLSGNSLIAPLSRSIKPVTLHLIACDTEFSDEKGN 60
QY 61 MYVLGKDKLCECAEIQGKPTQLQKEKNIMD 93
Db 61 MYVLGKDKLCECAEIQGKPTQLQKGGSD 93

RESULT 4
ID 090HA7 PRELIMINARY; PRT; 158 AA.
AC 090HA7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE FILI EPSILON.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kudin M., Garika K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL: AF201831; AAF25211.1;
DR HSP: P18510; IIRA.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR SMART: SM00125; IL1; 1.
SO SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;

Query Match 47.1%; Score 385; DB 4; Length 158;
Best Local Similarity 49.0%; Pred. No. 8.1e-32;
Matches 71; Conservative 29; Mismatches 45; Indels 0; Gaps 0;

QY 9 PKSYAIRDSRQWVWVLSGNSLIAPLSRSIKPVTLHLIACDTEFSDEKGNVYLGIG 68
Db 10 POGSIOIDINHRVWVLODQTLVAVPRKDRMSPVYIALISCHNHYETLEKDRNPITLGLNG 69
QY 69 KDLCECAEIQGKPTQLQKEKNIMDLYEKKAKQPFLEFHNKEGTSVSQSVYSGWFI 128
Db 70 LNLCECAEIQGKPTQLQKEKNIMDLYEKKAKQPFLEFHNKEGTSVSQSVYSGWFI 129

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OY 129 TSTTSGPIFLTKRGITNTNTNPFYL 153
DB 130 VSSEGGCPILITQELGKANTDFGL 154

RESULT 5
O9NZH8 PRELIMINARY; PRT; 169 AA.
AC 09NZH8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).
GN IL1E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20209405; PubMed-10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-PRIMARY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IFN;
RA Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT related protein 2; response is antagonized by IL-1d.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF200492; AAF69248.1; -
DR EMBL; AF206696; AAG35670.1; -
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;

Query Match 42.2%; Score 345.5; DB 4; Length 169;
Best local Similarity 45.0%; Pred. No. 9.8e-28;
Matches 68; Conservative 29; Mismatches 53; Indels 1; Gaps 1;

OY 4 QREAPKSYAIRDSRQMWVLSGNSLIAPLSRSIKPVTLLIACRDFEFSKRGNNMY 63
DB 17 QSMCKPITGTRINDINQOQWVTLQOGNLVAVPRSDSVTPVTAVITCKYPEALQGRDPT 76
OY 64 LGTIGKGLCLFCALIQGKPTQLQLEKNIMDYVEKKAOKPFLFFHNKESSTVSFOSVSP 123
DB 77 LGGINPEKCLCEVGEPTQLQLEKQIMDYQGEPEVKKPFLFYAKKIGRTLSVAVP 136

OY 124 GWFATSTTSGPIFLTKRGITNTNPFYL 154
DB 137 DMFIASSKRD-QPIITLSELGKSYNTAFELN 166

RESULT 6
O9JIA2 PRELIMINARY; PRT; 160 AA.
AC 09JIA2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON) (INTERLEUKIN 1
DE SUPERAMILY 1, EPSILON).
GN FILI OR IL1E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chordata; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20209405; PubMed-10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT related protein 2; response is antagonized by IL-1d.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-EMBRYO;
RA MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glaser C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita K., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald I., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Sessa T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AF200493; AAF69249.1; -
DR EMBL; AF206697; AAG35671.1; -
DR EMBL; AK004061; BAB23147.1; -
DR MGD; MGI:1859324; Fil1.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 160 AA; 18015 MW; AA0434D68FF62F4A CRC64;

Query Match 35.9%; Score 293.5; DB 11; Length 160;
Best local Similarity 37.7%; Pred. No. 2e-22;
Matches 58; Conservative 31; Mismatches 62; Indels 3; Gaps 1;

OY 1 MNPQRE--AAPKSYAIRDSRQMWVLSGNSLIAPLSRSIKPVTLLIACRDFEFSKE 57
DB 1 MNKEKELRAASPSLRHVODLSRWVLIQNNITLTVPRKEQTPVPTITLLPCQYDITLFTN 60
OY 58 KGNMNYLGIGKGLCLFCALIQGKPTQLQLEKNIMDYVEKKAOKPFLFFHNKESSTVSF 117
DB 61 RGDPTYGVOVRPMSCLECTKQGEQPVTLQLEGNITMKNKKEPKYASLFIYHKKSITSTF 120

OY 118 QSVSYPGMFTATSTTSGPIFLTKRGITNTNPF 151
DB 121 ESAAPGWFIAVCSGSPILITQELGIFITDF 154

RESULT 7
O9UHA6 PRELIMINARY; PRT; 192 AA.
AC 09UHA6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

```

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE FILI ZETA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20092888; PubMed=10625660;
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garck K.E.,
 RA Sims J.E.;
 RT "Four New Members Expand the IL-1 Superfamily.";
 RL J. Biol. Chem. 275:1169-1175(2000).
 DR EMBL: AF201832; AAF25212.1;
 DR HSP: P18510; 1ITN
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR SMART: SM00125; IL1; 1.
 SQ SEQUENCE 192 AA; 21543 MW; 4AF584C81802F612 CRC64;

Query Match 28.0%; Score 229; DB 4; Length 192;
 Best Local Similarity 34.8%; Pred. No. 1e-15;
 Matches 47; Conservative 33; Mismatches 51; Indels 4; Gaps 3;

OY 9 PKSYAIRDSROMVWVLSGNSLIAPLSRSIKPYTLHLACRDTFSDKEKGMVYLGIG 68
 DB 31 PKFSIHDOHKLVLDSGNLIAVPDKNYIRPEIFPALA-SLSASAEKSPILLGVSK 89
 OY 69 KDLCLCAEIOGK--PTLOLKEKNIMDLVEKK-AQKPLFFHNKSGTSVFQSVSPGM 125
 DB 90 GECFLYCDKDGQSHPSLOLKEKIMKLAQKESARRPFIFYRAQVGSNMLESAAHPGM 149
 OY 126 FIATSTTSGOPIFLT 140
 DB 150 FICTSCNCPVGV 164

RESULT 8
 ID Q9NZH6 PRELIMINARY; PRT; 218 AA.
 AC Q9NZH6;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE INTERLEUKIN-1 HOMOLOG 4 (IL-1X PROTEIN) (INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM A).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=FETAL LUNG, FETAL TESTIS, FETAL B-CELL, AND FETAL COLON;
 RX MEDLINE=20209405; PubMed=10744718;
 RA Kumar S., McDonnell P.C., Lohr R., Tierney L., Tzimas M.N.,
 RA Griswold D.E., Capper E.A., Tai-Singer R., Wells G.I., Doyle M.L.,
 RA Young P.R.;
 RT "Identification and initial characterization of four novel members of the interleukin-1 family.";
 RL J. Biol. Chem. 275:10308-10314(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON CARCINOMA;
 RA Manoj P.P., Mantovani A., Muzio M.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Pan G., Rissler P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,
 RA Lewis L., Eigenbrodt C., Henzle W.J., Vandlen R., Filvaroff E.;
 RT "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-1R.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF200496; AAF69252.1;
 DR EMBL: AF167368; AAG29344.1;
 DR EMBL: AF251118; AAG14420.1;
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR SMART: SM00125; IL1; 1.
 SQ SEQUENCE 218 AA; 24126 MW; 96E089310D2CEAF68 CRC64;

Query Match 28.0%; Score 229; DB 4; Length 218;
 Best Local Similarity 34.8%; Pred. No. 1.2e-15;
 Matches 47; Conservative 33; Mismatches 51; Indels 4; Gaps 3;

OY 9 PKSYAIRDSROMVWVLSGNSLIAPLSRSIKPYTLHLACRDTFSDKEKGMVYLGIG 68
 DB 57 PKFSIHDOHKLVLDSGNLIAVPDKNYIRPEIFPALA-SLSASAEKSPILLGVSK 115
 OY 69 KDLCLCAEIOGK--PTLOLKEKNIMDLVEKK-AQKPLFFHNKSGTSVFQSVSPGM 125
 DB 116 GECFLYCDKDGQSHPSLOLKEKIMKLAQKESARRPFIFYRAQVGSNMLESAAHPGM 175
 OY 126 FIATSTTSGOPIFLT 140
 DB 176 FICTSCNCPVGV 190

RESULT 9
 ID Q9HBF3 PRELIMINARY; PRT; 218 AA.
 AC Q9HBF3;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan G., Rissler P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,
 RA Lewis L., Eigenbrodt C., Henzle W.J., Vandlen R., Filvaroff E.;
 RT "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-1R.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF251119; AAG14421.1;
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR ProDom: PD002536; Interleukin_1; 1.
 DR SMART: SM00125; IL1; 1.
 SQ SEQUENCE 218 AA; 24138 MW; 76E09C35093DEA63 CRC64;

Query Match 28.0%; Score 229; DB 4; Length 218;
 Best Local Similarity 34.8%; Pred. No. 1.2e-15;
 Matches 47; Conservative 33; Mismatches 51; Indels 4; Gaps 3;

OY 9 PKSYAIRDSROMVWVLSGNSLIAPLSRSIKPYTLHLACRDTFSDKEKGMVYLGIG 68
 DB 57 PKFSIHDOHKLVLDSGNLIAVPDKNYIRPEIFPALA-SLSASAEKSPILLGVSK 115
 OY 69 KDLCLCAEIOGK--PTLOLKEKNIMDLVEKK-AQKPLFFHNKSGTSVFQSVSPGM 125
 DB 116 GECFLYCDKDGQSHPSLOLKEKIMKLAQKESARRPFIFYRAQVGSNMLESAAHPGM 175
 OY 126 FIATSTTSGOPIFLT 140
 DB 176 FICTSCNCPVGV 190

RESULT 10
 ID Q9UBH0 PRELIMINARY; PRT; 155 AA.

[illegible]

QY 57 EKNMNYLIGIKGDLCECAEIQGK--PTIQLEKKNIMLYVEKK-AQKPLFFHNKES 113
 DB 64 EKGSPILLGYSKGEFLCYCDKDGSHPSQLKKEKMKLAQKESARRPFIYRAQVGS 123
 QY 114 TSVFQSVSYPCWFIAITSTSGQPIFLT 140
 DB 124 WNMLESAAHPGWFICTSCNCEPVGYT 150

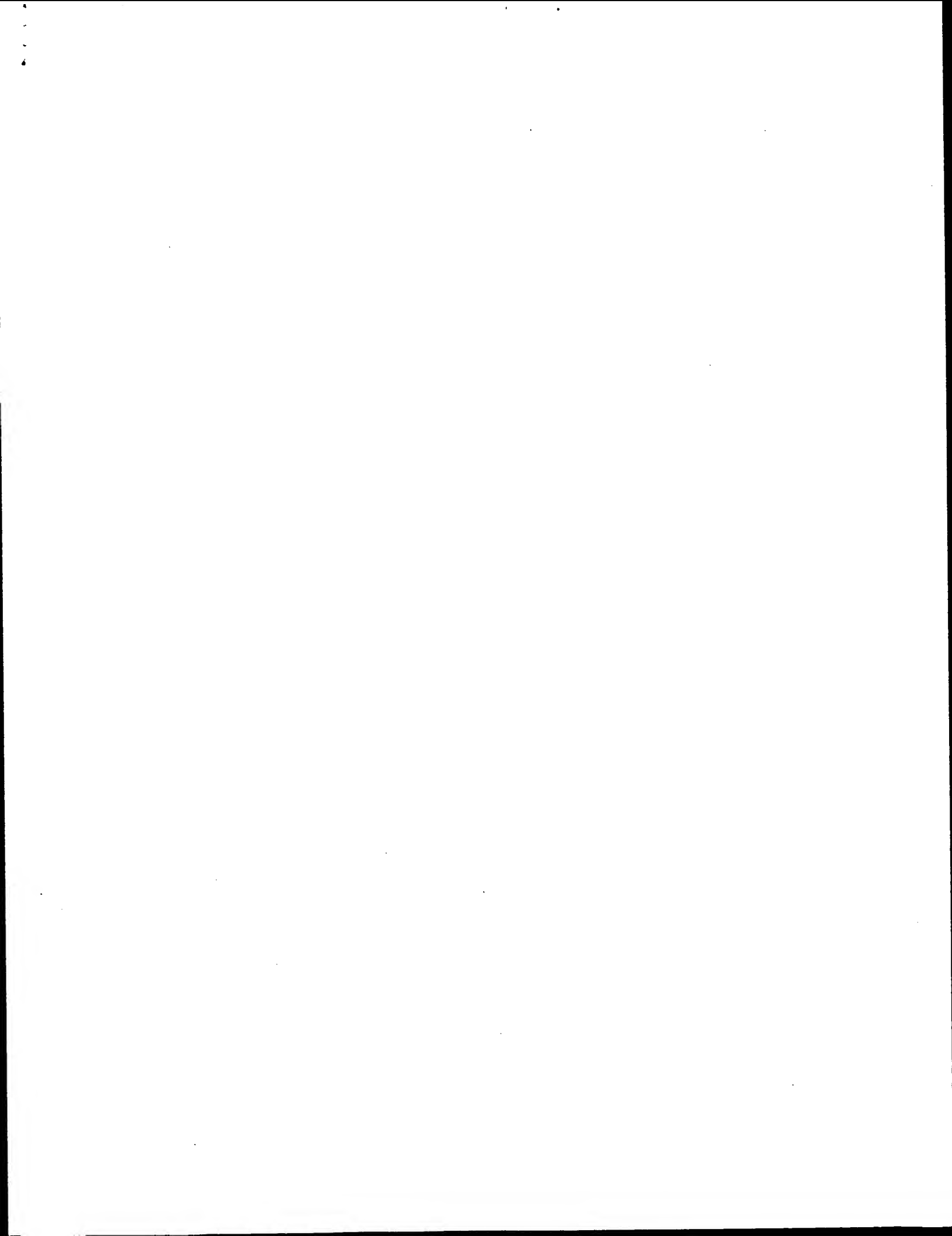
RESULT 15

014628 PRELIMINARY; PRT: 180 AA.
 AC 014628;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE INTRACELLULAR IL-1 RECEPTOR ANTAGONIST TYPE II.
 GN IL-1RN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95355865; PubMed=7629520;
 RA Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
 RA Introna M., Mantovani A., Colotta F.;
 RA "Cloning and characterization of a new isoform of the interleukin 1
 RT receptor antagonist."
 RL J. Exp. Med. 182:623-628(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97146044; PubMed=8992991;
 RA Jenkins J.K., Diron R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
 RA Arend W.P., Smith M.F., Jr.;
 RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
 RT and inducible regulatory regions."
 RL J. Immunol. 158:748-755(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Slightom J.L.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X84348; CAA59087.1; -;
 DR EMBL: U65590; AAB92269.1; -;
 DR HSSP: P18510; IIRP
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 SO SEQUENCE 180 AA; 19897 MW; 624A1574C234229 CRC64;

Query Match 22.2%; Score 182; DB 4; Length 180;
 Best Local Similarity 27.9%; Pred. No. 6, 1e-11;
 Matches 46; Conservative 27; Mismatches 64; Indels 28; Gaps 4;

QY 4 OREAPKSYAIRDSROMVWVLSGNLIAPLSR-----SIKPYTLHLIACRDTEFS 54
 DB 33 KSSSMQAFRIWDVQKTFYLRNNQLVAGYLOGPNVLEKIDVVPIDEPHAL----- 84
 QY 55 DKENGMYLIGIKGDLCECAEIQGKPTIQLEKKNIMLYVEKKAKQKPLFFHNKESG 114
 DB 85 -----FLGIHGKMKLSCVKSQDETIRQLQLEAVNITDLSNRKQDKRFAFIRSDSGPT 136
 QY 115 SVFQSVSYPCWFIAITSTSGQPIFLTK--ERGITNNTNPFYLDSE 157
 DB 137 TSFSAACPGWFLCTAMEADQPVSLTNMDEGVM-VTKFYFOEDE 180

Search completed: May 10, 2002, 09:12:37
 Job time: 112 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 10, 2002, 09:09:50 ; Search time 12.56 Seconds
(without alignments)
281.291 Million cell updates/sec

Title: US-09-723-676-2
Perfect score: 818
Sequence: 1 MNPQREAPKSYAIRDSRQ.....FLTKRGITNTNPLYDSVE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	452	55.3	164	2	US-08-939-300-2
2	345.5	42.2	169	2	US-08-790-032-2
3	345.5	42.2	169	3	US-09-069-619-2
4	262	32.0	71	2	US-08-939-300-4
5	200.5	24.5	155	4	US-09-417-455-5
6	195.5	23.9	178	3	US-09-000-630C-21
7	195.5	23.9	178	3	US-08-862-730C-21
8	195.5	23.9	178	4	US-09-417-455-9
9	187	22.9	185	3	US-09-128-155-18
10	186	22.7	153	3	US-08-798-414-2
11	186	22.7	153	4	US-09-131-247-2
12	186	22.7	153	4	US-09-131-247-4
13	186	22.7	388	4	US-09-131-247-16
14	186	22.7	389	4	US-09-131-247-14
15	183.5	22.4	178	3	US-09-000-630C-23
16	183.5	22.4	178	4	US-08-862-730C-23
17	183.5	22.4	178	4	US-09-417-455-10
18	183.5	22.3	115	3	US-09-128-155-5
19	183.5	22.3	115	3	US-09-128-155-9
20	182.5	22.3	115	3	US-09-128-155-13
21	182.5	22.3	136	3	US-09-128-155-11
22	182.5	22.3	167	3	US-09-128-155-7
23	182.5	22.3	178	3	US-09-128-155-2
24	182	22.2	156	1	US-08-476-860-10
25	182	22.2	156	2	US-08-910-733-10
26	182	22.2	156	2	US-08-910-884-10
27	182	22.2	159	1	US-08-459-811-2

28	182	22.2	159	2	US-08-484-598-2	Sequence 2, Appl1
29	182	22.2	159	2	US-08-092-092-2	Sequence 2, Appl1
30	182	22.2	159	2	US-08-459-814-2	Sequence 2, Appl1
31	182	22.2	159	2	US-08-425-232-2	Sequence 2, Appl1
32	182	22.2	159	2	US-08-471-227-3	Sequence 2, Appl1
33	182	22.2	159	2	US-08-479-140-2	Sequence 2, Appl1
34	182	22.2	159	3	US-08-477-143-2	Sequence 2, Appl1
35	182	22.2	159	4	US-09-417-455-14	Sequence 14, Appl1
36	182	22.2	177	1	US-08-423-655-2	Sequence 2, Appl1
37	182	22.2	177	2	US-08-809-185-2	Sequence 2, Appl1
38	182	22.2	177	3	US-09-000-630C-20	Sequence 20, Appl1
39	182	22.2	177	3	US-08-862-730C-20	Sequence 20, Appl1
40	182	22.2	177	3	US-09-128-155-14	Sequence 14, Appl1
41	182	22.2	177	4	US-09-417-455-30	Sequence 30, Appl1
42	182	22.2	180	1	US-08-476-860-13	Sequence 13, Appl1
43	182	22.2	180	2	US-08-910-733-13	Sequence 13, Appl1
44	182	22.2	180	2	US-08-910-884-13	Sequence 13, Appl1
45	178.5	21.8	177	3	US-09-000-630C-22	Sequence 22, Appl1

ALIGNMENTS

RESULT 1
US-08-939-300-2
Sequence 2, Application US/08939300
Patent No. 5945310
GENERAL INFORMATION:
APPLICANT: Young, Peter R.
APPLICANT: James, Ian E.
TITLE OF INVENTION: Connor, Janice R.
TITLE OF INVENTION: A No. 5945310e1 Member of the IL-1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: RATTNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939, 300
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046, 957
FILING DATE: May 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23, 031
REFERENCE/DOCKET NUMBER: GH-70018
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-939-300-2
Query Match 55.3%; Score 452; DB 2; Length 164;
Best Local Similarity 94.6%; Pred. No. 1.6e-43;


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Query Match Similarity      32.0%; Score 262; DB 2; Length 71;
Best Local Similarity      77.9%; Pred. No. 1.5e-22;
Matches 53; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY      2  NPGREAAPKSYAIRDSRQWVWVLSGNSLIAPLSRSIKPYTLHLIACRDTEFSDEKRGKM 61
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      3  NGRQHPXPMLFY--NSXQWVWVLSGNXLIAPLSRSIKPYTLHLIACRDTEFSDEKRGKM 60
QY      62  VYLGIKKG 69
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      61  VYLGIKKG 68

RESULT 5
US-09-417-455-5
; Sequence 5, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13

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Query Match	24.5%;	Score 200.5;	DB 4;	Length 155;
Best Local Similarity	35.1%;	Pred. No. 3,8e-15;		
Matches	54;	Conservative	24;	Mismatches 61;
				Indels 15;
				Gaps 6;

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1      RESULT      6
2      US-09-000-630C-21
3      ; Sequence 21, Application US/09000630C
4      ; Patent No. 6018029
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Fuller, Gerald M.
7      ; APPLICANT: Fuentes, Nelson L.
8      ; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
9      ; TITLE OF INVENTION: Antagonist
10     ; NUMBER OF SEQUENCES: 27
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESSSEE: Douglas C Murdoch/ Bradley, Arant, Rose & White
13     ; STREET: 2001 Park Place, Suite 1400
14     ; CITY: Birmingham
15     ; STATE: Alabama
16     ; COUNTRY: USA
17     ; ZIP: 35203-2736
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Diskette, 3.50 inch,
20     ; COMPUTER: IBM compatible
21     ; OPERATING SYSTEM: Microsoft Windows
22     ; SOFTWARE: Wordperfect 6.0
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/09/000,630C
25     ; FILING DATE:
26     ; PRIOR APPLICATION DATA:
27     ; APPLICATION NUMBER: 08/862,730
28     ; FILING DATE:
29     ; INFORMATION FOR SEQ ID NO.: 21:
30     ; SEQUENCE CHARACTERISTICS:
31     ; LENGTH: 178 amino acids
32     ; TYPE: amino acid
33     ; STRANDEDNESS: single
34     ; TOPOLOGY: linear
35     ; MOLECULE TYPE: mouse IL-1ra sequence
36     ; US-09-000-630C-21

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Query Match      23.9%; Score 195.5; DB 3; Length 178;
Best Local Similarity 33.6%; Pred. No. 1,7e-14;
Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;

QY 4 QREAPKSAIRDSRQWVWVLSGNSLIAAPL-SRSIK-----PYTLHLIACRDTERRS 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 KRCKMQAFRIWDTNOKTFYLRNNQLIAGYLOGPNIKLECKIDWPIDLH----- 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 55 DKEGNMNYLIGIKGKDLCPAEIQGKPTLQLEKNIMDLVEKKAOKPFLFFHNKESG 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 81 -----SVFLGHHGKLCCLCAKSGDDIKQLQLEEVNITDLSKNKEEDKRFTFIRSEK 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 SVFQSVSYPGWFIATSTTSGQPIFLT 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 TSFESAACPGWFLCTTLEADRPVSLT 160

RESULT 7
US-08-862-730C-21
; Sequence 21, Application US/08862730C
; Patent No. 6063600
; GENERAL INFORMATION:
; APPLICANT: Puller, Gerald M.
; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Douglas C. Murdock / Bradley, Arant, Rose & White
; STREET: 2001 Park Place, Suite 1400
; CITY: Birmingham
; STATE: Alabama
; COUNTRY: USA
; ZIP: 35203-2736
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; OPERATING SYSTEM: Microsoft Windows
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,730C
; FILING DATE: 5/23/97
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mouse IL-1ra sequence
; US-08-862-730C-21

Query Match      23.9%; Score 195.5; DB 3; Length 178;
Best Local Similarity 33.6%; Pred. No. 1,7e-14;
Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;

QY 4 QREAPKSAIRDSRQWVWVLSGNSLIAAPL-SRSIK-----PYTLHLIACRDTERRS 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 KRCKMQAFRIWDTNOKTFYLRNNQLIAGYLOGPNIKLECKIDWPIDLH----- 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 55 DKEGNMNYLIGIKGKDLCPAEIQGKPTLQLEKNIMDLVEKKAOKPFLFFHNKESG 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 81 -----SVFLGHHGKLCCLCAKSGDDIKQLQLEEVNITDLSKNKEEDKRFTFIRSEK 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 SVFQSVSYPGWFIATSTTSGQPIFLT 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 TSFESAACPGWFLCTTLEADRPVSLT 160

RESULT 8
US-09-417-455-9
; Sequence 9, Application US/09417455

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; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-417-455-9

Query Match      23.9%; Score 195.5; DB 4; Length 178;
Best Local Similarity 33.6%; Pred. No. 1,7e-14;
Matches 49; Conservative 23; Mismatches 49; Indels 25; Gaps 3;

QY 4 QREAPKSAIRDSRQWVWVLSGNSLIAAPL-SRSIK-----PYTLHLIACRDTERRS 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 KRCKMQAFRIWDTNOKTFYLRNNQLIAGYLOGPNIKLECKIDWPIDLH----- 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 55 DKEGNMNYLIGIKGKDLCPAEIQGKPTLQLEKNIMDLVEKKAOKPFLFFHNKESG 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 81 -----SVFLGHHGKLCCLCAKSGDDIKQLQLEEVNITDLSKNKEEDKRFTFIRSEK 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 SVFQSVSYPGWFIATSTTSGQPIFLT 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 TSFESAACPGWFLCTTLEADRPVSLT 160

RESULT 9
US-09-128-155-18
; Sequence 18, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 185

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; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
; FILE REFERENCE: A-365F
; CURRENT APPLICATION NUMBER: US/09/131,247
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/055,185
; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: PCT/US 97/02131
; EARLIER FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRF
; ORGANISM: Human
; US-09-131-247-4

Query Match      22.7%; Score 186; DB 4; Length 153;
Best Local Similarity 29.4%; Pred. No. 1.6e-13;
Matches 50; Conservative 22; Mismatches 68; Indels 30; Gaps 5;

OY 1 MNPQREAPKSAIR--DSROMVWVLSGNSLIAPLSR-----SIKPYTLHLIACR 49
DB 1 MRPSGRKSSKMQAFRIWDVNOKTFYLRNNOVLVAGYLOGPNVNLLEKIDVPIEPHAL--- 57
OY 50 DTEFSDKEKGNMNYLIGIKGDLCLFCFAEIOGKPTQLQLEKNIMDLVEKKAQKPFLEFHN 109
DB 58 -----FLGIHGKMKLSCVKSQDETRLOLEAVNITDLSENRKODKRFAPFIRS 104
OY 110 KEGTSVFOGVSYPGWFIATSTSGOPIFLTK--ERGITTNTNFYLDSE 157
DB 105 DSGPTTFSFESACPGWFLCTAMEADQPVSLTNMPDEGVA-VTKFYFQDE 153

RESULT 13
US-09-131-247-16
; Sequence 16, Application US/09131247
; Patent No. 6294170
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Hershenson, Susan
; APPLICANT: Bevilacqua, Michael P.
; APPLICANT: Collins, David S.
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
; FILE REFERENCE: A-365F
; CURRENT APPLICATION NUMBER: US/09/131,247
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/055,185
; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: PCT/US 97/02131
; EARLIER FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 388
; TYPE: PRF
; ORGANISM: Human
; US-09-131-247-16

Query Match      22.7%; Score 186; DB 4; Length 388;
Best Local Similarity 29.4%; Pred. No. 5.9e-13;
Matches 50; Conservative 22; Mismatches 68; Indels 30; Gaps 5;

OY 1 MNPQREAPKSAIR--DSROMVWVLSGNSLIAPLSR-----SIKPYTLHLIACR 49
DB 1 MRPSGRKSSKMQAFRIWDVNOKTFYLRNNOVLVAGYLOGPNVNLLEKIDVPIEPHAL--- 57
OY 50 DTEFSDKEKGNMNYLIGIKGDLCLFCFAEIOGKPTQLQLEKNIMDLVEKKAQKPFLEFHN 109
DB 58 -----FLGIHGKMKLSCVKSQDETRLOLEAVNITDLSENRKODKRFAPFIRS 104
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OY 110 KEGTSVFOGVSYPGWFIATSTSGOPIFLTK--ERGITTNTNFYLDSE 157
DB 105 DSGPTTFSFESACPGWFLCTAMEADQPVSLTNMPDEGVA-VTKFYFQDE 153

RESULT 14
US-09-131-247-14
; Sequence 14, Application US/09131247
; Patent No. 6294170
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Hershenson, Susan
; APPLICANT: Bevilacqua, Michael P.
; APPLICANT: Collins, David S.
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
; FILE REFERENCE: A-365F
; CURRENT APPLICATION NUMBER: US/09/131,247
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 60/055,185
; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: PCT/US 97/02131
; EARLIER FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 389
; TYPE: PRF
; ORGANISM: Human
; US-09-131-247-14

Query Match      22.7%; Score 186; DB 4; Length 389;
Best Local Similarity 29.4%; Pred. No. 5.9e-13;
Matches 50; Conservative 22; Mismatches 68; Indels 30; Gaps 5;

OY 1 MNPQREAPKSAIR--DSROMVWVLSGNSLIAPLSR-----SIKPYTLHLIACR 49
DB 237 MRPSGRKSSKMQAFRIWDVNOKTFYLRNNOVLVAGYLOGPNVNLLEKIDVPIEPHAL--- 293
OY 50 DTEFSDKEKGNMNYLIGIKGDLCLFCFAEIOGKPTQLQLEKNIMDLVEKKAQKPFLEFHN 109
DB 294 -----FLGIHGKMKLSCVKSQDETRLOLEAVNITDLSENRKODKRFAPFIRS 340
OY 110 KEGTSVFOGVSYPGWFIATSTSGOPIFLTK--ERGITTNTNFYLDSE 157
DB 341 DSGPTTFSFESACPGWFLCTAMEADQPVSLTNMPDEGVA-VTKFYFQDE 389

RESULT 15
US-09-000-630C-23
; Sequence 23, Application US/09000630C
; Patent No. 6018029
; GENERAL INFORMATION:
; APPLICANT: Fuller, Gerald M.
; APPLICANT: Fuentes, Nelson L.
; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Douglas C Murdock / Bradley, Arant, Rose & White
; STREET: 2001 Park Place, Suite 1400
; CITY: Birmingham
; STATE: Alabama
; COUNTRY: USA
; ZIP: 35203-2736
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
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